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(21) International Application Number: PCT/US99/15838 (22) International Filing Date: 14 July 1999 (14.07.99) (30) Priority Data: <table border="0"> <tr> <td>09/115,453</td> <td>14 July 1998 (14.07.98)</td> <td>US</td> </tr> <tr> <td>09/116,134</td> <td>14 July 1998 (14.07.98)</td> <td>US</td> </tr> <tr> <td>09/159,822</td> <td>23 September 1998 (23.09.98)</td> <td>US</td> </tr> <tr> <td>09/159,812</td> <td>23 September 1998 (23.09.98)</td> <td>US</td> </tr> <tr> <td>09/232,880</td> <td>15 January 1999 (15.01.99)</td> <td>US</td> </tr> <tr> <td>09/232,149</td> <td>15 January 1999 (15.01.99)</td> <td>US</td> </tr> <tr> <td>09/288,946</td> <td>9 April 1999 (09.04.99)</td> <td>US</td> </tr> </table> (71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US). (72) Inventors: DILLON, Davin, Clifford; 21607 N.E. 24th Street, Redmond, WA 98053 (US). HARLOCKER, Susan, Louise; 6203 20th Avenue N.W., Seattle, WA 98107 (US). YUQIU, Jiang; 5001 South 232nd Street, Kent, WA 98032 (US). XU, Jiangchun; 15805 S.E. 43rd Place, Bellevue, WA 98006 (US). MITCHAM, Jennifer, Lynn; 16677 Northeast 88th Street, Redmond, WA 98052 (US).	09/115,453	14 July 1998 (14.07.98)	US	09/116,134	14 July 1998 (14.07.98)	US	09/159,822	23 September 1998 (23.09.98)	US	09/159,812	23 September 1998 (23.09.98)	US	09/232,880	15 January 1999 (15.01.99)	US	09/232,149	15 January 1999 (15.01.99)	US	09/288,946	9 April 1999 (09.04.99)	US	(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia, 701 Fifth Avenue, Seattle, WA 98104-7092 (US). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
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(54) Title: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER (57) Abstract <p>Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate tumor protein, or mRNA encoding such a protein, in a sample are also provided.</p>																						

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COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER

TECHNICAL FIELD

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides comprising at least a portion of a prostate tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for prevention and treatment of prostate cancer, and for the diagnosis and monitoring of such cancers.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the diagnosis and therapy of cancer, such as prostate cancer. In one aspect, the present

invention provides polypeptides comprising at least a portion of a prostate tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; (b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and (c) complements of any of the sequence of (a) or (b). In certain specific embodiments, such a polypeptide comprises at least a portion, or variant thereof, of a tumor protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a prostate tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and a non-specific immune response enhancer.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a prostate tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a non-specific immune response enhancer.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a non-specific immune response enhancer.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a prostate tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T-cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited

above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be prostate cancer.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic

kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate tumor polypeptide P502S, as compared to control fibroblasts. The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate tumor polypeptide P502S. In each case, the number of γ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/*neu*.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate tumor polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8⁺ cell line (3A-1) for a representative prostate tumor antigen (P501S). Figure 6A shows the results of a ⁵¹Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12
SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16
SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1
SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9
SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4
SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17
SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17
SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12
SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12
SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862
SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862
SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13
SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13
SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19
SEQ ID NO: 17 is the determined 5' cDNA sequence for J1-19
SEQ ID NO: 18 is the determined 3' cDNA sequence for J1-25
SEQ ID NO: 19 is the determined 5' cDNA sequence for J1-25
SEQ ID NO: 20 is the determined 5' cDNA sequence for J1-24
SEQ ID NO: 21 is the determined 3' cDNA sequence for J1-24
SEQ ID NO: 22 is the determined 5' cDNA sequence for K1-58
SEQ ID NO: 23 is the determined 3' cDNA sequence for K1-58
SEQ ID NO: 24 is the determined 5' cDNA sequence for K1-63
SEQ ID NO: 25 is the determined 3' cDNA sequence for K1-63
SEQ ID NO: 26 is the determined 5' cDNA sequence for L1-4
SEQ ID NO: 27 is the determined 3' cDNA sequence for L1-4
SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14
SEQ ID NO: 29 is the determined 3' cDNA sequence for L1-14
SEQ ID NO: 30 is the determined 3' cDNA sequence for J1-12
SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16
SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21
SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48
SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55
SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2
SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6
SEQ ID NO: 37 is the determined 3' cDNA sequence for N1-1858
SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860
SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861

SEQ ID NO: 40 is the determined 3' cDNA sequence for N1-1864
SEQ ID NO: 41 is the determined cDNA sequence for P5
SEQ ID NO: 42 is the determined cDNA sequence for P8
SEQ ID NO: 43 is the determined cDNA sequence for P9
SEQ ID NO: 44 is the determined cDNA sequence for P18
SEQ ID NO: 45 is the determined cDNA sequence for P20
SEQ ID NO: 46 is the determined cDNA sequence for P29
SEQ ID NO: 47 is the determined cDNA sequence for P30
SEQ ID NO: 48 is the determined cDNA sequence for P34
SEQ ID NO: 49 is the determined cDNA sequence for P36
SEQ ID NO: 50 is the determined cDNA sequence for P38
SEQ ID NO: 51 is the determined cDNA sequence for P39
SEQ ID NO: 52 is the determined cDNA sequence for P42
SEQ ID NO: 53 is the determined cDNA sequence for P47
SEQ ID NO: 54 is the determined cDNA sequence for P49
SEQ ID NO: 55 is the determined cDNA sequence for P50
SEQ ID NO: 56 is the determined cDNA sequence for P53
SEQ ID NO: 57 is the determined cDNA sequence for P55
SEQ ID NO: 58 is the determined cDNA sequence for P60
SEQ ID NO: 59 is the determined cDNA sequence for P64
SEQ ID NO: 60 is the determined cDNA sequence for P65
SEQ ID NO: 61 is the determined cDNA sequence for P73
SEQ ID NO: 62 is the determined cDNA sequence for P75
SEQ ID NO: 63 is the determined cDNA sequence for P76
SEQ ID NO: 64 is the determined cDNA sequence for P79
SEQ ID NO: 65 is the determined cDNA sequence for P84
SEQ ID NO: 66 is the determined cDNA sequence for P68
SEQ ID NO: 67 is the determined cDNA sequence for P80
SEQ ID NO: 68 is the determined cDNA sequence for P82
SEQ ID NO: 69 is the determined cDNA sequence for U1-3064
SEQ ID NO: 70 is the determined cDNA sequence for U1-3065
SEQ ID NO: 71 is the determined cDNA sequence for V1-3692
SEQ ID NO: 72 is the determined cDNA sequence for 1A-3905
SEQ ID NO: 73 is the determined cDNA sequence for V1-3686
SEQ ID NO: 74 is the determined cDNA sequence for R1-2330
SEQ ID NO: 75 is the determined cDNA sequence for 1B-3976
SEQ ID NO: 76 is the determined cDNA sequence for V1-3679

SEQ ID NO: 77 is the determined cDNA sequence for 1G-4736
SEQ ID NO: 78 is the determined cDNA sequence for 1G-4738
SEQ ID NO: 79 is the determined cDNA sequence for 1G-4741
SEQ ID NO: 80 is the determined cDNA sequence for 1G-4744
SEQ ID NO: 81 is the determined cDNA sequence for 1G-4734
SEQ ID NO: 82 is the determined cDNA sequence for 1H-4774
SEQ ID NO: 83 is the determined cDNA sequence for 1H-4781
SEQ ID NO: 84 is the determined cDNA sequence for 1H-4785
SEQ ID NO: 85 is the determined cDNA sequence for 1H-4787
SEQ ID NO: 86 is the determined cDNA sequence for 1H-4796
SEQ ID NO: 87 is the determined cDNA sequence for 1I-4807
SEQ ID NO: 88 is the determined cDNA sequence for 1I-4810
SEQ ID NO: 89 is the determined cDNA sequence for 1I-4811
SEQ ID NO: 90 is the determined cDNA sequence for 1J-4876
SEQ ID NO: 91 is the determined cDNA sequence for 1K-4884
SEQ ID NO: 92 is the determined cDNA sequence for 1K-4896
SEQ ID NO: 93 is the determined cDNA sequence for 1G-4761
SEQ ID NO: 94 is the determined cDNA sequence for 1G-4762
SEQ ID NO: 95 is the determined cDNA sequence for 1H-4766
SEQ ID NO: 96 is the determined cDNA sequence for 1H-4770
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SEQ ID NO: 104 is the determined cDNA sequence for 1D-4304
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SEQ ID NO: 106 is the determined cDNA sequence for 1D-4280
SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12 (also referred to as P504S)
SEQ ID NO: 108 is the predicted amino acid sequence for F1-12
SEQ ID NO: 109 is the determined full length cDNA sequence for J1-17
SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12
SEQ ID NO: 111 is the determined full length cDNA sequence for N1-1862
SEQ ID NO: 112 is the predicted amino acid sequence for J1-17

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SEQ ID NO: 133 is the determined cDNA sequence for P156
SEQ ID NO: 134 is the determined cDNA sequence for P157
SEQ ID NO: 135 is the determined cDNA sequence for P166
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SEQ ID NO: 165 is the determined cDNA sequence for P195
SEQ ID NO: 166 is the determined cDNA sequence for P196
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SEQ ID NO: 169 is the determined cDNA sequence for P235
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SEQ ID NO: 183 is the determined extended cDNA sequence for 1H-4774
SEQ ID NO: 184 is the determined extended cDNA sequence for 1H-4781
SEQ ID NO: 185 is the determined extended cDNA sequence for 1H-4785
SEQ ID NO: 186 is the determined extended cDNA sequence for 1H-4787

SEQ ID NO: 187 is the determined extended cDNA sequence for 1H-4796
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SEQ ID NO: 196 is the determined extended cDNA sequence for 1H-4766
SEQ ID NO: 197 is the determined 3' cDNA sequence for 1H-4770
SEQ ID NO: 198 is the determined 3' cDNA sequence for 1H-4771
SEQ ID NO: 199 is the determined extended cDNA sequence for 1H-4772
SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-4309
SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-4278
SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-4288
SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-4283
SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-4304
SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-4296
SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-4280
SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd
SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con
SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev
SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd
SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev
SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd
SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev
SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd
SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev
SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd
SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev
SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd
SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev
SEQ ID NO: 220 is the determined cDNA sequence for 8-h11rev
SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd
SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev
SEQ ID NO: 223 is the determined cDNA sequence for P509S

SEQ ID NO: 224 is the determined cDNA sequence for P510S
SEQ ID NO: 225 is the determined cDNA sequence for P703DE5
SEQ ID NO: 226 is the determined cDNA sequence for 9-A11
SEQ ID NO: 227 is the determined cDNA sequence for 8-C6
SEQ ID NO: 228 is the determined cDNA sequence for 8-H7
SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13
SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14
SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23
SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24
SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25
SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30
SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34
SEQ ID NO: 236 is the determined cDNA sequence for PTPN35
SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36
SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38
SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39
SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40
SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41
SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42
SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45
SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46
SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51
SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56
SEQ ID NO: 247 is the determined cDNA sequence for PTPN64
SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65
SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67
SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84
SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86
SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1
SEQ ID NO: 257 is the determined cDNA sequence for JP1F2
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2
SEQ ID NO: 259 is the determined cDNA sequence for JP1B1
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2

SEQ ID NO: 261 is the determined cDNA sequence for JP1D3
SEQ ID NO: 262 is the determined cDNA sequence for JP1A4
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6
SEQ ID NO: 266 is the determined cDNA sequence for JP1B5
SEQ ID NO: 267 is the determined cDNA sequence for JP1A6
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9
SEQ ID NO: 271 is the determined cDNA sequence for JP1C10
SEQ ID NO: 272 is the determined cDNA sequence for JP1A9
SEQ ID NO: 273 is the determined cDNA sequence for JP1F12
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11
SEQ ID NO: 276 is the determined cDNA sequence for JP1C11
SEQ ID NO: 277 is the determined cDNA sequence for JP1C12
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2
SEQ ID NO: 281 is the determined cDNA sequence for JP8H1
SEQ ID NO: 282 is the determined cDNA sequence for JP8H2
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3
SEQ ID NO: 286 is the determined cDNA sequence for JP8G4
SEQ ID NO: 287 is the determined cDNA sequence for JP8B6
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6
SEQ ID NO: 289 is the determined cDNA sequence for JP8F5
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8
SEQ ID NO: 291 is the determined cDNA sequence for JP8C7
SEQ ID NO: 292 is the determined cDNA sequence for JP8D7
SEQ ID NO: 293 is the determined cDNA sequence for P8D8
SEQ ID NO: 294 is the determined cDNA sequence for JP8E7
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8
SEQ ID NO: 297 is the determined cDNA sequence for JP8B10

SEQ ID NO: 298 is the determined cDNA sequence for JP8C10
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9
SEQ ID NO: 302 is the determined cDNA sequence for JP8H9
SEQ ID NO: 303 is the determined cDNA sequence for JP8C12
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12
SEQ ID NO: 307 is the determined cDNA sequence for P711P
SEQ ID NO: 308 is the determined cDNA sequence for P712P
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23
SEQ ID NO: 310 is the determined cDNA sequence for P774P
SEQ ID NO: 311 is the determined cDNA sequence for P775P
SEQ ID NO: 312 is the determined cDNA sequence for P715P
SEQ ID NO: 313 is the determined cDNA sequence for P710P
SEQ ID NO: 314 is the determined cDNA sequence for P767P
SEQ ID NO: 315 is the determined cDNA sequence for P768P
SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5
SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5
SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26
SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26
SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23
SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23
SEQ ID NO: 332 is the determined full length cDNA sequence for P509S
SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)
SEQ ID NO: 334 is the determined cDNA sequence for P714P
SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)
SEQ ID NO: 336 is the predicted amino acid sequence for P705P
SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10
SEQ ID NO: 338 is the amino acid sequence of the peptide p5
SEQ ID NO: 339 is the predicted amino acid sequence of P509S
SEQ ID NO: 340 is the determined cDNA sequence for P778P
SEQ ID NO: 341 is the determined cDNA sequence for P786P
SEQ ID NO: 342 is the determined cDNA sequence for P789P

SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo sapiens MM46 mRNA

SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA

SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin

SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)

SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)

SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)

SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteosome subunit p40

SEQ ID NO: 350 is the determined cDNA sequence for P777P

SEQ ID NO: 351 is the determined cDNA sequence for P779P

SEQ ID NO: 352 is the determined cDNA sequence for P790P

SEQ ID NO: 353 is the determined cDNA sequence for P784P

SEQ ID NO: 354 is the determined cDNA sequence for P776P

SEQ ID NO: 355 is the determined cDNA sequence for P780P

SEQ ID NO: 356 is the determined cDNA sequence for P544S

SEQ ID NO: 357 is the determined cDNA sequence for P745S

SEQ ID NO: 358 is the determined cDNA sequence for P782P

SEQ ID NO: 359 is the determined cDNA sequence for P783P

SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984

SEQ ID NO: 361 is the determined cDNA sequence for P787P

SEQ ID NO: 362 is the determined cDNA sequence for P788P

SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994

SEQ ID NO: 364 is the determined cDNA sequence for P781P

SEQ ID NO: 365 is the determined cDNA sequence for P785P

SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.

SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.

SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.

SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.

SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.

SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.

SEQ ID NO: 381 is the determined cDNA sequence for B716P.

SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.

SEQ ID NO: 383 is the predicted amino acid sequence for P711P.

SEQ ID NO: 384 is the cDNA sequence for P1000C.

SEQ ID NO: 385 is the cDNA sequence for CGI-82.

SEQ ID NO:386 is the cDNA sequence for 23320.

SEQ ID NO:387 is the cDNA sequence for CGI-69.

SEQ ID NO:388 is the cDNA sequence for L-iditol-2-dehydrogenase.

SEQ ID NO:389 is the cDNA sequence for 23379.

SEQ ID NO:390 is the cDNA sequence for 23381.

SEQ ID NO:391 is the cDNA sequence for KIAA0122.

SEQ ID NO:392 is the cDNA sequence for 23399.

SEQ ID NO:393 is the cDNA sequence for a previously identified gene.

SEQ ID NO:394 is the cDNA sequence for HCLBP.

SEQ ID NO:395 is the cDNA sequence for transglutaminase.

SEQ ID NO:396 is the cDNA sequence for a previously identified gene.

SEQ ID NO:397 is the cDNA sequence for PAP.

SEQ ID NO:398 is the cDNA sequence for Ets transcription factor PDEF.

SEQ ID NO:399 is the cDNA sequence for hTGR.

SEQ ID NO:400 is the cDNA sequence for KIAA0295.

SEQ ID NO:401 is the cDNA sequence for 22545.

SEQ ID NO:402 is the cDNA sequence for 22547.

SEQ ID NO:403 is the cDNA sequence for 22548.

SEQ ID NO:404 is the cDNA sequence for 22550.

SEQ ID NO:405 is the cDNA sequence for 22551.

SEQ ID NO:406 is the cDNA sequence for 22552.

SEQ ID NO:407 is the cDNA sequence for 22553.

SEQ ID NO:408 is the cDNA sequence for 22558.

SEQ ID NO:409 is the cDNA sequence for 22562.

SEQ ID NO:410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.

SEQ ID NO:412 is the cDNA sequence for 22568.

SEQ ID NO:413 is the cDNA sequence for 22570.

SEQ ID NO:414 is the cDNA sequence for 22571.
SEQ ID NO:415 is the cDNA sequence for 22572.
SEQ ID NO:416 is the cDNA sequence for 22573.
SEQ ID NO:417 is the cDNA sequence for 22573.
SEQ ID NO:418 is the cDNA sequence for 22575.
SEQ ID NO:419 is the cDNA sequence for 22580.
SEQ ID NO:420 is the cDNA sequence for 22581.
SEQ ID NO:421 is the cDNA sequence for 22582.
SEQ ID NO:422 is the cDNA sequence for 22583.
SEQ ID NO:423 is the cDNA sequence for 22584.
SEQ ID NO:424 is the cDNA sequence for 22585.
SEQ ID NO:425 is the cDNA sequence for 22586.
SEQ ID NO:426 is the cDNA sequence for 22587.
SEQ ID NO:427 is the cDNA sequence for 22588.
SEQ ID NO:428 is the cDNA sequence for 22589.
SEQ ID NO:429 is the cDNA sequence for 22590.
SEQ ID NO:430 is the cDNA sequence for 22591.
SEQ ID NO:431 is the cDNA sequence for 22592.
SEQ ID NO:432 is the cDNA sequence for 22593.
SEQ ID NO:433 is the cDNA sequence for 22594.
SEQ ID NO:434 is the cDNA sequence for 22595.
SEQ ID NO:435 is the cDNA sequence for 22596.
SEQ ID NO:436 is the cDNA sequence for 22847.
SEQ ID NO:437 is the cDNA sequence for 22848.
SEQ ID NO:438 is the cDNA sequence for 22849.
SEQ ID NO:439 is the cDNA sequence for 22851.
SEQ ID NO:440 is the cDNA sequence for 22852.
SEQ ID NO:441 is the cDNA sequence for 22853.
SEQ ID NO:442 is the cDNA sequence for 22854.
SEQ ID NO:443 is the cDNA sequence for 22855.
SEQ ID NO:444 is the cDNA sequence for 22856.
SEQ ID NO:445 is the cDNA sequence for 22857.
SEQ ID NO:446 is the cDNA sequence for 23601.
SEQ ID NO:447 is the cDNA sequence for 23602.
SEQ ID NO:448 is the cDNA sequence for 23605.
SEQ ID NO:449 is the cDNA sequence for 23606.
SEQ ID NO:450 is the cDNA sequence for 23612.

SEQ ID NO:451 is the cDNA sequence for 23614.
SEQ ID NO:452 is the cDNA sequence for 23618.
SEQ ID NO:453 is the cDNA sequence for 23622.
SEQ ID NO:454 is the cDNA sequence for folate hydrolase.
SEQ ID NO:455 is the cDNA sequence for LIM protein.
SEQ ID NO:456 is the cDNA sequence for a known gene.
SEQ ID NO:457 is the cDNA sequence for a known gene.
SEQ ID NO:458 is the cDNA sequence for a previously identified gene.
SEQ ID NO:459 is the cDNA sequence for 23045.
SEQ ID NO:460 is the cDNA sequence for 23032.
SEQ ID NO:461 is the cDNA sequence for 23054.
SEQ ID NOs:462-467 are cDNA sequences for known genes.
SEQ ID NOs:468-471 are cDNA sequences for P710P.
SEQ ID NO:472 is a cDNA sequence for P1001C.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer. The compositions described herein may include prostate tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a prostate tumor protein or a variant thereof. A "prostate tumor protein" is a protein that is expressed in prostate tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal tissue, as determined using a representative assay provided herein. Certain prostate tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with prostate cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human prostate tumor proteins. Sequences of polynucleotides encoding certain tumor proteins, or portions thereof, are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Sequences of polypeptides comprising at least a portion of a tumor protein are provided in SEQ ID NOs:112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

PROSTATE TUMOR PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a prostate tumor protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a prostate tumor protein. More preferably, a polynucleotide encodes an immunogenic portion of a prostate tumor protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a prostate tumor protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native prostate tumor protein or a portion thereof.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50,

in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenesis pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native prostate tumor protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to

the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a prostate tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as prostate tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion may be used to isolate a full length gene from a suitable library (*e.g.*, a prostate tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA-clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using

standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding at least a portion of a prostate tumor protein are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Isolation of these

polynucleotides is described below. Each of these prostate tumor proteins was overexpressed in prostate tumor tissue.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a prostate tumor protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (e.g., by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a prostate tumor polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a tumor protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (e.g., promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such

as inosine, queosine and wybutosine, as well as acetyl- methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors.. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

PROSTATE TUMOR POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a prostate tumor protein or a variant thereof, as described herein. As noted above, a "prostate tumor protein" is a protein that is expressed by prostate tumor cells. Proteins that are prostate tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with prostate cancer. Polypeptides as described herein may be of any length. Additional sequences derived from

the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a prostate tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native prostate tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native prostate tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native prostate tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein.

Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are

E. coli, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into

the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as

amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a prostate tumor protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a prostate tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a prostate tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a prostate tumor protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, urine and/or tumor biopsies) from

patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient

time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (e.g., covalently bonded) to a suitable monoclonal antibody either directly or indirectly (e.g., via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (e.g., a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and

thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a prostate tumor protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the CEPRATE™ system, available from CellPro Inc., Bothell WA (*see also* U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a prostate tumor polypeptide, polynucleotide encoding a prostate tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a prostate tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a prostate tumor polypeptide if the T cells kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.*, by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a prostate tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (*e.g.*, TNF or IFN-γ) is indicative of T cell activation (*see* Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience

(Greene 1998)). T cells that have been activated in response to a prostate tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Prostate tumor protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a prostate tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a prostate tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a prostate tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a prostate tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and a non-specific immune response enhancer. A non-specific immune response enhancer may be any substance that enhances an immune response to an exogenous antigen. Examples of non-specific immune response enhancers include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998,

and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described; for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or

preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6, IL-10 and TNF- β) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is

quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*) and based on the lack of differentiation markers of B cells (CD19 and CD20), T cells (CD3), monocytes (CD14) and natural killer cells (CD56), as determined using standard assays. Dendritic cells may, of course, be engineered to express specific cell-

surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80 and CD86).

APCs may generally be transfected with a polynucleotide encoding a prostate tumor protein (or portion or other variant thereof) such that the prostate tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the prostate tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that

provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as prostate cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein

may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 μ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such

a response can be monitored by establishing an improved clinical outcome (e.g., more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a prostate tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding

agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred

embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use prostate tumor polypeptides to

detect antibodies that bind to such polypeptides in a biological sample. The detection of such prostate tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a prostate tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a prostate tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with prostate tumor polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T-cell sample in the absence of prostate tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a prostate tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a prostate tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the prostate tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a prostate tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a prostate tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers

comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375 and 381. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple prostate tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a prostate tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a prostate tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a prostate tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a prostate tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of

H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor-expression-enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human

autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted

amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO: 73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and

prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional, studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that

F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression

in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatzis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. No significant homologies were found to the sequence of P1000C.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated

and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a portion of the P703P-gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the microarray technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable.

Increased expression of 8-F11 was seen in prostate tumor and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both micro-array technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR-subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues.

Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 5

FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 10 (SEQ ID NO: 340-349) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350-365.

EXAMPLE 6

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

Mice expressing the transgene for human HLA A2.1 (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 100µg of P2S#12 and 120µg of an I-A^b binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at 6×10^6 cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL), 2×10^{-5} M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later, cells (5×10^5 /ml) were restimulated with 2.5×10^6 /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were

restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2.1 expressing) transduced with P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2.1 molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 $\mu\text{g/ml}$ were added to cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes, CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2.1 were immunized as described by Theobald et al. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5 μg of P1S #10 and 120 μg of an I-A^b binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh. Cells were then resuspended at 6×10^6 cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed (2 $\mu\text{g/ml}$ P1S#10 and 10mg/ml β 2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7 $\mu\text{g/ml}$ dextran sulfate and 25 $\mu\text{g/ml}$ LPS for 3 days). Six days later cells (5×10^5 /ml) were restimulated with 2.5×10^6 /ml peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly

basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

EXAMPLE 7

ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE TUMOR POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

Human CD8⁺ T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8⁺ T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a γ -interferon ELISPOT assay (see Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on 10^4 fibroblasts in the presence of 3 μ g/ml human β_2 -microglobulin and 1 μ g/ml P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the fibroblasts were treated with 10 ng/ml γ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a γ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of γ -interferon spots with increasing numbers of T

cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

EXAMPLE 8

PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION WITH A PROSTATE ANTIGEN

The prostate tumor antigen L1-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100 µg VR10132-P501S either intramuscularly or intradermally. The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at least one naturally processed A2-restricted CTL epitope.

EXAMPLE 9

GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND STIMULATION TECHNIQUES WITH PROSTATE TUMOR ANTIGEN

Using *in vitro* whole-gene priming with P501S-retrovirally transduced autologous fibroblasts (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon-γ ELISPOT analysis as described above. Using a panel of HLA-mismatched fibroblast lines transduced with P501S, these CTL lines were shown to be restricted HLA-A2 class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3 µg/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8+ T cells were isolated using a magnetic bead system, and

priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S. Following four stimulation cycles, CD8+ T cell lines were identified that specifically produced interferon- γ when stimulated with P501S-transduced autologous fibroblasts. The P501S-specific activity could be sustained by the continued stimulation of the cultures with P501S-transduced fibroblasts in the presence of IL-15. A panel of HLA-mismatched fibroblast lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- γ in an ELISPOT assay, the P501S specific response was shown to be restricted by HLA-A2. These results demonstrate that a CD8+ CTL response to P501S can be elicited.

EXAMPLE 10

IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN A PROSTATE TUMOR ANTIGEN

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2 transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of P703P transduced target cells expressing either HLA-A2Kb or HLA-A2. Specifically, HLA-A2 transgenic mice were immunized subcutaneously in the footpad with 100 μ g of p5 peptide together with 140 μ g of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS-blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with p5 peptide and cultured with GM-CSF and IL-4 together with CD8+ T cell enriched PBMC. CTL lines were restimulated on a weekly basis

with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures, CTL recognition of p5-pulsed target cells was demonstrated.

EXAMPLE 11

EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN IN PROSTATE

Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that B305D is highly expressed in breast tumor, prostate tumor, normal prostate tumor and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach).

EXAMPLE 12

ELICITATION OF PROSTATE TUMOR ANTIGEN-SPECIFIC CTL RESPONSES IN HUMAN BLOOD

This Example illustrates the ability of a prostate tumor antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GM-CSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8⁺ cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles, CD8⁺ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to

express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays (^{51}Cr release) and interferon-gamma production (Interferon-gamma Elispot; *see above* and Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). The results of these assays are presented in Figures 6A and 6B.

EXAMPLE 13

IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

Table I
Summary of Prostate Tumor Antigens

Known Genes	Previously identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-Iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang(23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	

transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-iditol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate

tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97% of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

EXAMPLE 14

IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate tumor antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups, Plus (normal prostate and prostate tumor libraries, and breast cell lines, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table II
Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones found in the Plus and Other group libraries only; no expression detected in the Minus group; Type 3- EST clones found in the Plus, Minus and Other group libraries, but the expression in the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones found in Plus, Minus and Other group libraries, but the expression in the Plus group is higher than the expression in the Minus group. This analysis identified 4,345 breast clusters (see Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

The inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor cDNA was at least three times the level in normal prostate cDNA) were identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NOs:401-453, with certain novel sequences shown in SEQ ID NOs:407, 413, 416-419, 422, 426, 427 and 450.

Table IV
Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P

403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57

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439	22851	PAP
440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

EXAMPLE 15

FURTHER IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NOs:454-467. Of these sequences SEQ ID NOs:459-461 correspond to novel genes. The others (SEQ ID NOs:454-458 and 461-467) correspond to known sequences.

EXAMPLE 16

FURTHER CHARACTERIZATION OF PROSTATE TUMOR ANTIGEN P710P

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates. Nylon membrane filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic ABI Sequencer. Four sequences were obtained, and are presented in SEQ ID NOs:468-471.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the present invention is not limited except as by the appended claims.

CLAIMS

1. An isolated polypeptide comprising at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in any one of SEQ ID NOs: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472;

(b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and

(c) complements of any of the sequence of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 108, 112, 113, 114, 172, 176, 178, 327, 329, 331, 339 and 383.

4. An isolated polynucleotide encoding at least 15 amino acid residues of a prostate tumor protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434,

435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

7. An isolated polynucleotide comprising a sequence that hybridizes, under moderately stringent conditions, to a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector comprising a polynucleotide according to any one of claims 4-7.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An expression vector comprising a polynucleotide according claim 8.

12. A host cell transformed or transfected with an expression vector according to claim 11.

13. A pharmaceutical composition comprising a polypeptide according to claim 1, in combination with a physiologically acceptable carrier.

14. A vaccine comprising a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

15. A vaccine according to claim 14, wherein the non-specific immune response enhancer is an adjuvant.

16. A vaccine according to claim 14, wherein the non-specific immune response enhancer induces a predominantly Type I response.

17. A pharmaceutical composition comprising a polynucleotide according to claim 4, in combination with a physiologically acceptable carrier.

18. A vaccine comprising a polynucleotide according to claim 4, in combination with a non-specific immune response enhancer.

19. A vaccine according to claim 18, wherein the non-specific immune response enhancer is an adjuvant.

20. A vaccine according to claim 18, wherein the non-specific immune response enhancer induces a predominantly Type I response.

21. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a prostate tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472 or a complement of any of the foregoing polynucleotide sequences.

22. A pharmaceutical composition comprising an antibody or fragment thereof according to claim 18, in combination with a physiologically acceptable carrier.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

26. A vaccine according to claim 25, wherein the non-specific immune response enhancer is an adjuvant.

27. A vaccine according to claim 25, wherein the non-specific immune response enhancer induces a predominantly Type I response.

28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

29. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

30. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polynucleotide according to claim 4, and thereby inhibiting the development of a cancer in the patient.

31. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antibody or antigen-binding fragment thereof according to claim 21, and thereby inhibiting the development of a cancer in the patient.

32. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

33. A method according to claim 32, wherein the antigen-presenting cell is a dendritic cell.

34. A method according to any one of claims 29-32, wherein the cancer is prostate cancer.

35. A fusion protein comprising at least one polypeptide according to claim 1.

36. A fusion protein according to claim 35, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

37. A fusion protein according to claim 35, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

38. A fusion protein according to claim 35, wherein the fusion protein comprises an affinity tag.

39. An isolated polynucleotide encoding a fusion protein according to claim 35.

40. A pharmaceutical composition comprising a fusion protein according to claim 32, in combination with a physiologically acceptable carrier.

41. A vaccine comprising a fusion protein according to claim 35, in combination with a non-specific immune response enhancer.

42. A vaccine according to claim 41, wherein the non-specific immune response enhancer is an adjuvant.

43. A vaccine according to claim 41, wherein the non-specific immune response enhancer induces a predominantly Type I response.

44. A pharmaceutical composition comprising a polynucleotide according to claim 40, in combination with a physiologically acceptable carrier.

45. A vaccine comprising a polynucleotide according to claim 40, in combination with a non-specific immune response enhancer.

46. A vaccine according to claim 45, wherein the non-specific immune response enhancer is an adjuvant.

47. A vaccine according to claim 45, wherein the non-specific immune response enhancer induces a predominantly Type I response.

48. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 40 or claim 44.

49. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 41 or claim 45.

50. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and

(ii) complements of the foregoing polynucleotides;
wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the prostate tumor protein from the sample.

51. A method according to claim 50, wherein the biological sample is blood or a fraction thereof.

52. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 50.

53. A method for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of:

- (i) a polypeptide according to claim 1;
 - (ii) a polypeptide encoded by a polynucleotide comprising a sequence provided in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
 - (iii) a polynucleotide encoding a polypeptide of (i) or (ii); and/or
 - (iv) an antigen presenting cell that expresses a polypeptide of (i) or (ii);
- under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

54. An isolated T cell population, comprising T cells prepared according to the method of claim 53.

55. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 54.

56. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

- (i) a polypeptide according to claim 1;
- (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
- (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
- (iv) an antigen-presenting-cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T-cells, and thereby inhibiting the development of a cancer in the patient.

57. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

- (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:
 - (i) a polypeptide according to claim 1;
 - (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
 - (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
 - (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate;

- (b) cloning at least one proliferated cell; and
- (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

58. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and

(ii) complements of the foregoing polynucleotides;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

59. A method according to claim 58, wherein the binding agent is an antibody.

60. A method according to claim 59, wherein the antibody is a monoclonal antibody.

61. A method according to claim 58, wherein the cancer is prostate cancer.
62. A method for monitoring the progression of a cancer in a patient, comprising the steps of:
- (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;
 - (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
 - (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
 - (d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.
63. A method according to claim 62, wherein the binding agent is an antibody.
64. A method according to claim 63, wherein the antibody is a monoclonal antibody.
65. A method according to claim 62, wherein the cancer is a prostate cancer.
-
66. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:
- (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;
 - (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

67. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

68. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

69. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

70. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

71. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

72. A diagnostic kit, comprising:

(a) one or more antibodies according to claim 21; and

(b) a detection reagent comprising a reporter group.

73. A kit according to claim 72, wherein the antibodies are immobilized on a solid support.

74. A kit according to claim 73, wherein the solid support comprises nitrocellulose, latex or a plastic material.

75. A kit according to claim 72, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

76. A kit according to claim 72, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

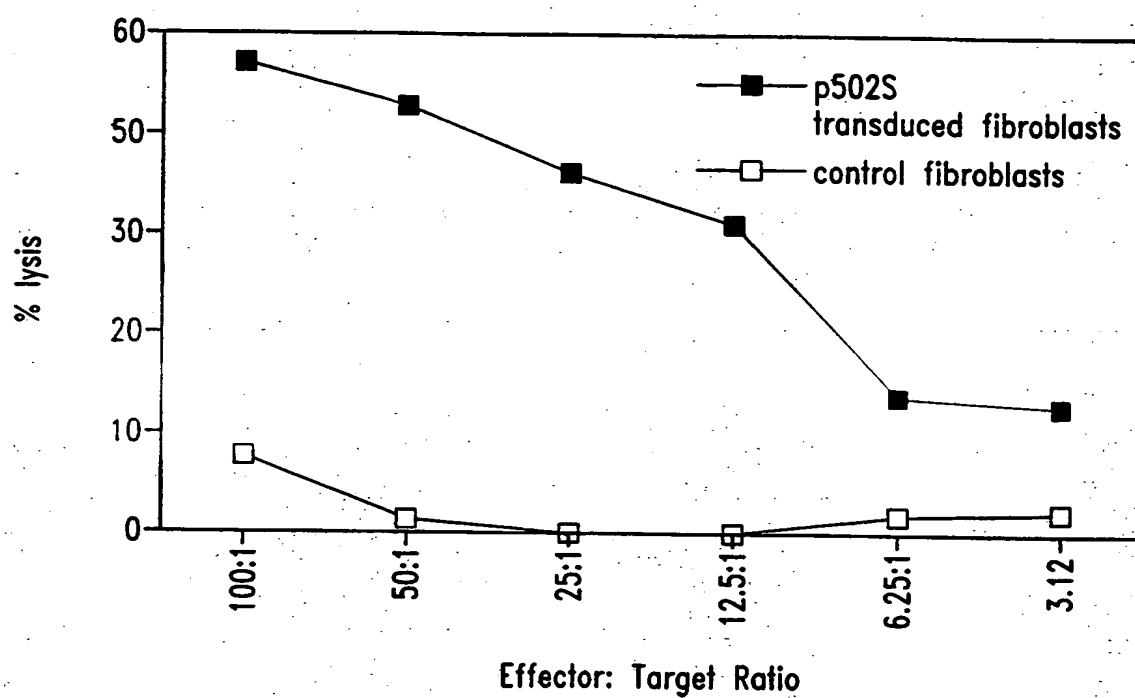
77. An oligonucleotide comprising 10 to 40 nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotides.

78. A oligonucleotide according to claim 77, wherein the oligonucleotide comprises 10-40 nucleotides recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

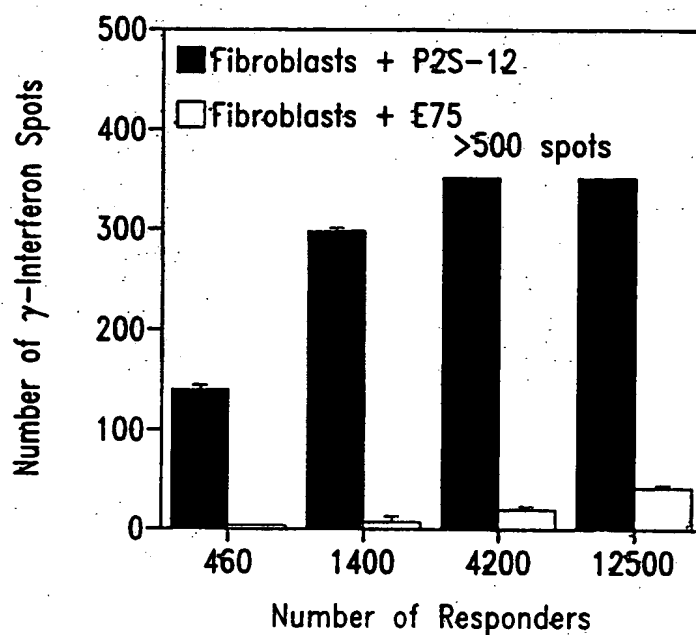
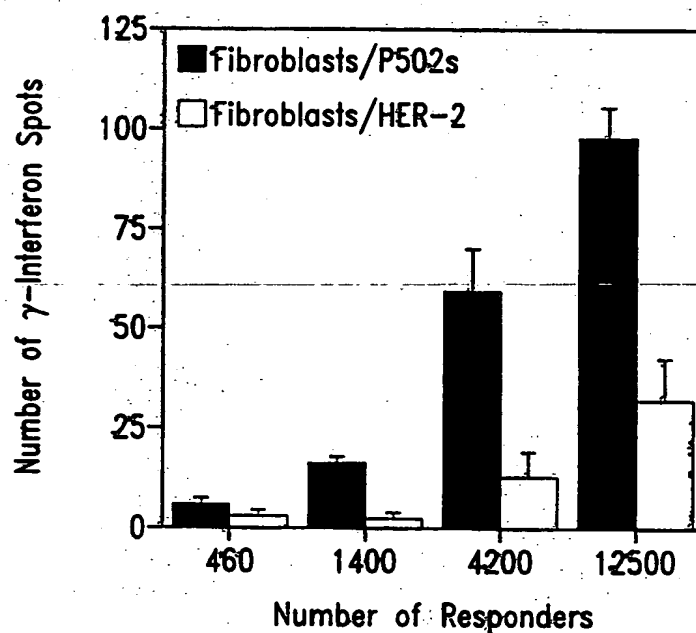
79. A diagnostic kit, comprising:

- (a) an oligonucleotide according to claim 77; and
- (b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

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*Fig. 1*

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*Fig. 2A**Fig. 2B*

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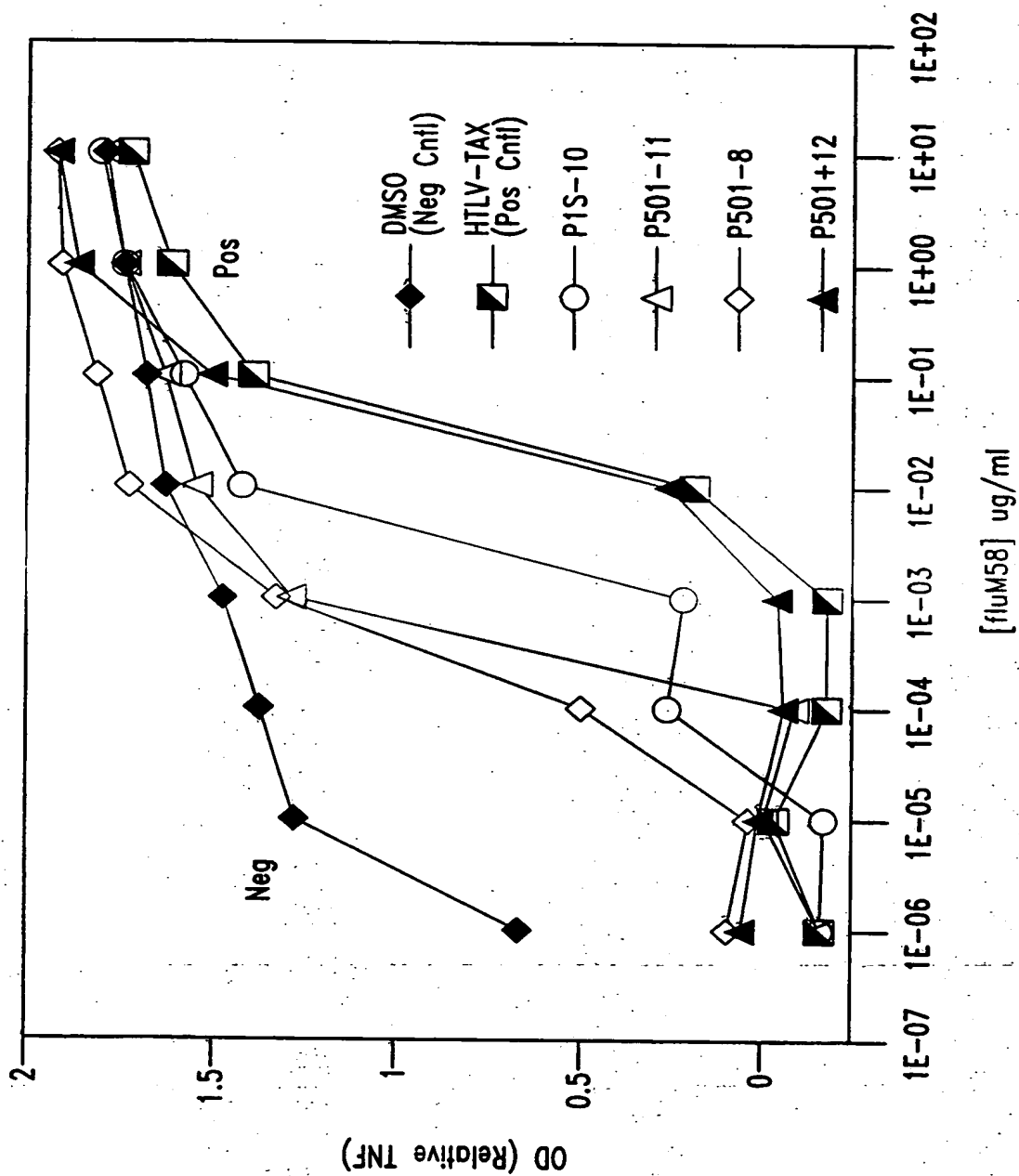
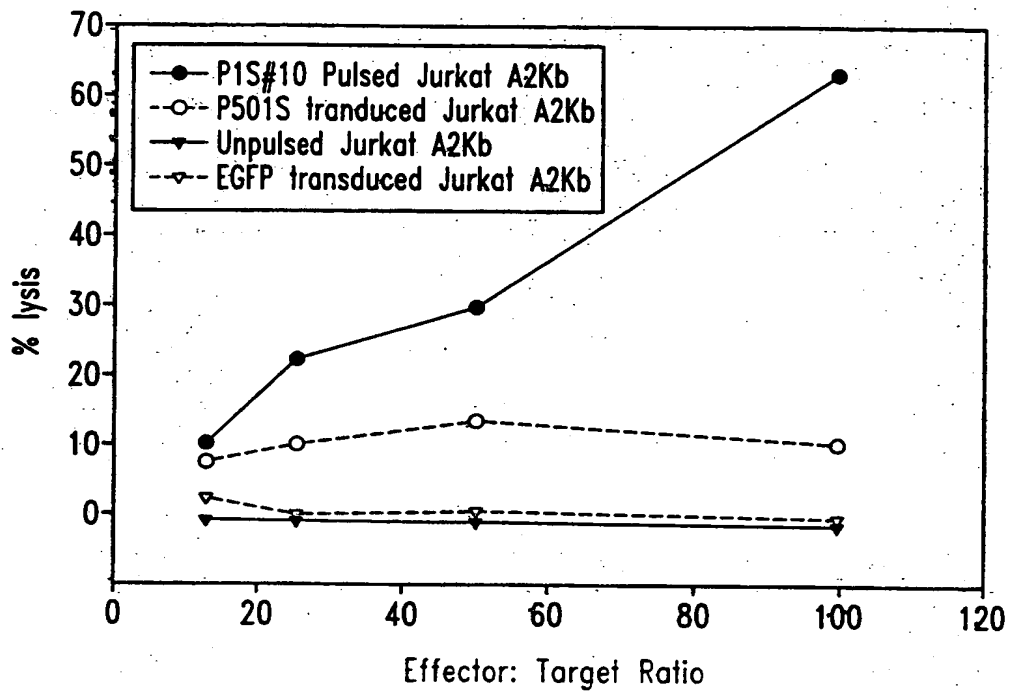
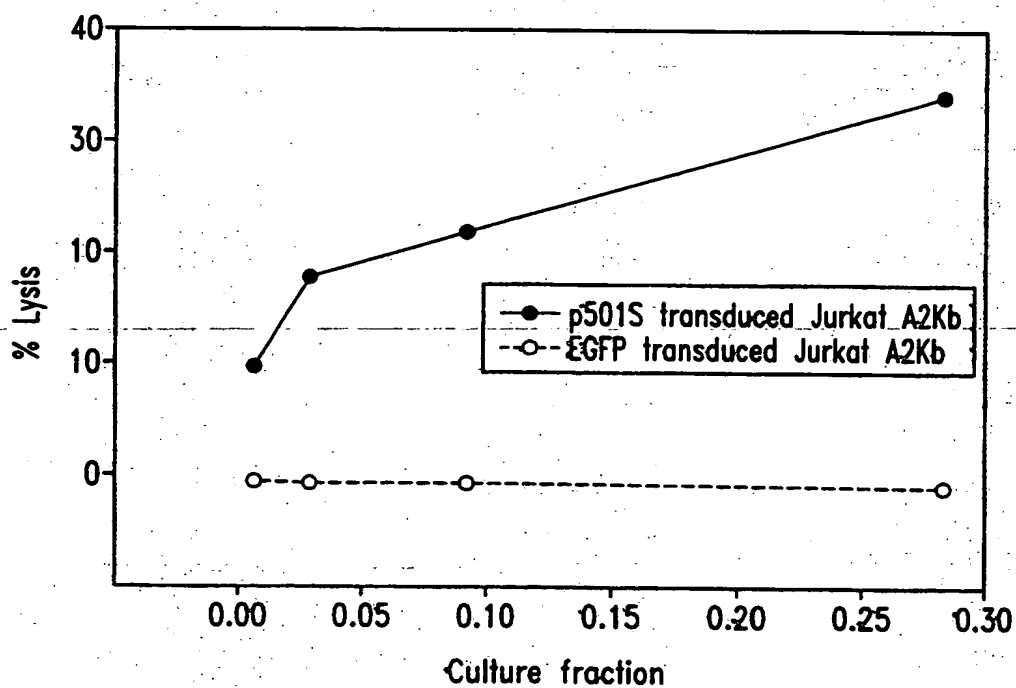
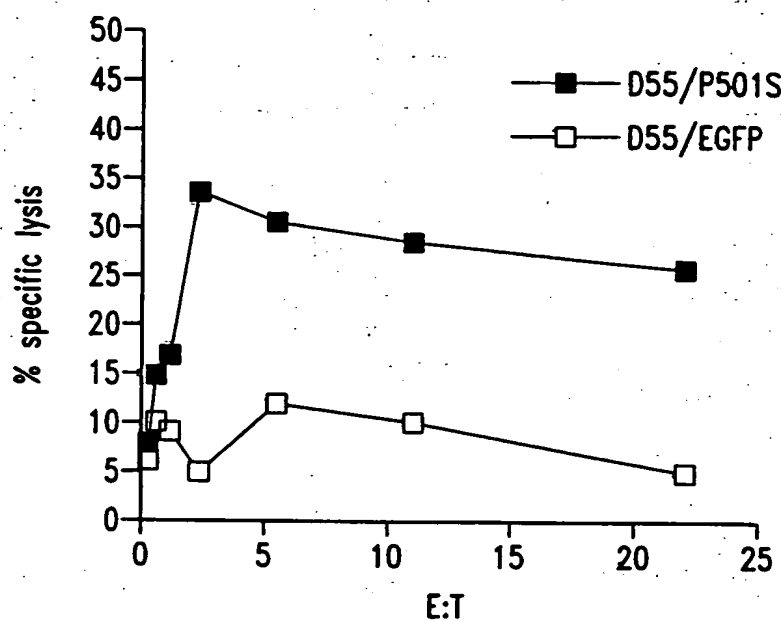
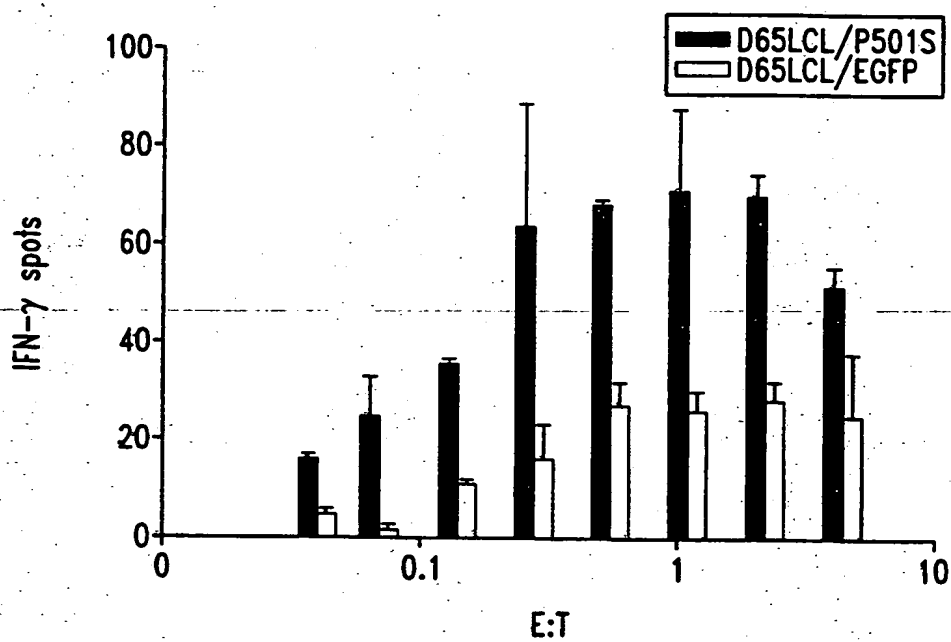


Fig. 3

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*Fig. 4**Fig. 5*

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*Fig. 6**Fig. 7*

SEQUENCE LISTING

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tcctcaaaaag	tcagaaccgg	agtcacacag	gcattctgtgc	cgtcaaagat	ttgacaccac	180
tctgccttcg	tcttctttgc	aaatacatct	gcaaacttet	tcttcatttc	tgccaatca	240
tccatgctca	tctgattggg	aagttcatca	gacttttagtc	canntccttt	gatcagcagc	300
tcgtagaact	ggggttctat	tgctccaaca	gccatgaatt	ccccatctgc	tgtcctgtaa	360
gtcgtataga	aaggtgctcc	accatccaac	atgttctgtc	ctcgaggggg	ggcccggtag	420
ccaattcgcc	ctatantgag	tcgtattacg	cgcgctcact	ggccgctcgtt	ttacaacgct	480
gtgactggga	aaaccctggg	cgttaccaac	ttaatcgctt	tgacgacat	ccccctttcg	540
ccagctgggc	gtaatancca	aaaggccccg	accgatcgcc	cttccaacag	ttgcgcacct	600
gaatgggnaa	atgggacccc	cctgttaccg	cgcattnaac	ccccgcnggg	tttngttgtt	660
acccccacnt	nnaccgctta	cactttgcca	gcgccttanc	gcccgcctccc	tttenccttt	720
cttcccttcc	tttencnccn	ctttcccccg	gggtttcccc	cntcaaacc	cna	773

<210> 4

<211> 828

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(828)

<223> n = A,T,C or G

<400> 4

cctcctgagt	cctactgacc	tgtgctttct	ggtgtggagt	ccagggctgc	taggaaaagg	60
aatgggcaga	cacaggtgta	tgccaatgtt	tctgaaatgg	gtataatttc	gtcctctcct	120
tcggaacact	ggctgtctct	gaagacttct	cgctcagttt	cagtgaggac	acacacaaag	180
acgtgggtga	ccatgttgtt	tgtgggggtgc	agagatggga	gggggtggggc	ccaccctgga	240
agagtggaca	gtgacacaag	gtggacactc	tctacagatc	actgaggata	agctggagcc	300
acaatgcatg	aggcacacac	acagcaaggga	tgacnctgta	aacatagccc	acgctgtcct	360

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gngggcactg ggaagcctan atnaggocgt gagcanaaag aaggggagga tccactagtt 420
ctanagcggc cgccaccgcg gtgganctcc ancttttgtt cccttttagtg agggttaatt 480
gcgcgcttgg cntaatcatg gtcatanctn ttctctgtgt gaaattgtta tccgctcaca 540
attccacaca acatacganc cggaaacata aantgtaaac ctgggggtgcc taatgantga 600
ctaactcaca ttaattgcgt tgcgctcact gcccgctttc caatcnggaa acctgtcttg 660
ccncttgcat tnatgaatcn gccaaccccc ggggaaaagc gtttgcgctt tgggcgctct 720
tccgcttctt cncctantta ntccctnenc tcggctcatt cggtcgngc aaaccgggtc 780
accnctcca aaggggggtat tccgggttcc ccnaatccgg gganancc 828

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<210> 5
 <211> 834
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(834)
 <223> n = A,T,C or G

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<400> 5
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agttttaatt gcatccaaag tactaacaaa aactctagca atcaagaatg gcagcatgtt 120
attttataac aatcaacacc tgtggctttt aaaatttggg tttcataaga taatttatac 180
tgaagtaaat ctagccatgc ttttaaaaaa tgctttaggc cactccaagc ttggcagtta 240
acatttggca taaacaataa taaaacaatc acaatttaac aaataacaaa tacaacattg 300
taggccataa tcatatacag tataaggaaa aggtggtagt gttgagtaag cagttattag 360
aatagaatac cttggcctct atgcaaatat gtctagacac tttgattcac tcagccctga 420
cattcagttt tcaaagtagg agacagggtc tacagtatca ttttacagtt tccaacacat 480
tgaaaacaag tagaaaatga tgagttgatt tttattaatg cattacatcc tcaagagtta 540
tcaccaaccc ctcagttata aaaaattttc aagttatatt agtcatataa cttgggtgtgc 600
ttattttaaa ttagtgctaa atggattaag tgaagacaac aatgggtccc taatgtgatt 660
gatattgggc atttttaoca gcttctaaat ctnaactttc aggtctttga actggaacat 720
tgnatnacag tgttccanag ttncaaccta ctggaacatt acagtgtgct tgattcaaaa 780
tgttattttg ttaaaaatta aattttaacc tgggtgaaaa ataatttgaa atna 834

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<210> 6
 <211> 818
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(818)
 <223> n = A,T,C or G

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<400> 6
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aaccacatct acaaaaatgcc agtatcaggc ggcggtctcg aagccaaagt gatgtttgga 120
tgtaaaagtga aatattagtt ggcggatgaa gcagatagtg aggaaagtgt agccaataat 180
gacgtgaagt ccgtggaagc ctgtggctac aaaaaatgtt gagocgtaga tgcggtcgga 240
aatggtgaag ggagactcga agtactctga ggcttctagg aggttaaaat agagaccag 300
taaaattgta ataagcagt cttgaattat ttggtttcgg ttgttttcta ttagactatg 360
gtgagctcag gtgattgata ctctgatgc gagtaatacg gatgtgttta ggagtgggac 420
ttctagggga tttagcgggg tgatgcctgt tggggggcag tgccctccta gtgggggggt 480
aggggctagg ctggagtggg aaaaggctca gaaaaatcct gcgaagaaaa aaacttctga 540

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ggtaataaat	aggattatcc	cgtatcgaag	gccttttttg	acagggtggtg	tgtggtggcc	600
ttggtatgtg	ctttctcgtg	ttacatcgcg	ccatcattgg	tatatggtta	gtgtgttggg	660
ttantanggc	ctantatgaa	gaacttttgg	antggaatta	aatcaatngc	ttggccggaa	720
gtcattanga	nggctnaaaa	ggccctgtta	ngggtctggg	ctnggtttta	cccnacccat	780
ggaatncncc	ccccggacna	ntgnatccct	attcttaa			818

<210> 7

<211> 817

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(817)

<223> n = A,T,C or G

<400> 7

tttttttttt	tttttttttt	tggctctaga	gggggtagag	gggggtgctat	agggtaaata	60
cgggccctat	ttcaaagatt	tttaggggaa	ttaattctag	gacgatgggt	atgaaactgt	120
ggtttgctcc	acagatttca	gagcattgac	cgtagtatac	ccccggtcgt	gtagcgggtga	180
aagtggtttg	gttttagacgt	ccgggaattg	catctgtttt	taagcctaata	gtggggacag	240
ctcatgagtg	caagacgtct	tgtgatgtaa	ttattatacn	aatgggggct	tcaatcgga	300
gtactactcg	attgtcaacg	tcaaggagtc	gcaggtcgcc	tggttctagg	aataatgggg	360
gaagtatgta	ggaattgaag	attaatccgc	cgtagtcggt	gttctctctag	gttcaatacc	420
attggtggcc	aattgatttg	atggtaaggg	gagggatcgt	tgaactcgtc	tgttatgtaa	480
aggatncctt	ngggatggga	aggcnatnaa	ggactangga	tnaatggcgg	gcangatatt	540
tcaaacngtc	tctanttcct	gaaacgtctg	aaatgttaat	aanaattaan	tttngttatt	600
gaatnttng	gaaaagggct	tacaggacta	gaaaccaaata	angaaaanta	atnntaangg	660
cnttatcntn	aaaggtnata	accnctccta	tnatcccacc	caatngnatt	ccccacncnn	720
acnattggat	nccccanttc	canaaaanggc	cnccccccg	tgnannccnc	ctttgttcc	780
cttnantgan	ggttattcnc	ccctngcntt	atcance			817

<210> 8

<211> 799

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(799)

<223> n = A,T,C or G

<400> 8

catttcggg	tttactttct	aaggaaagcc	gagcggaagc	tgctaacgtg	ggaatcgggtg	60
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ctgaagcgca	cgtcccagaa	ggtggacttg	gcactgaaac	agctgggaca	catccgcgag	180
tacgaacagc	gcctgaaagt	gctggagcgg	gaggtccagc	agtgtagccg	cgtcctgggg	240
tgggtggccg	angcctganc	cgtctgcct	tgctgcccc	angtgggccc	ccacccccctg	300
acctgcttg	gtccaaacac	tgagccctgc	tggcggaactt	caagganaac	ccccacangg	360
ggattttgct	cctanantaa	ggctcatctg	ggcctcgccc	ccccacactg	gttggccttg	420
tctttgngt	gagccccatg	tccatctggg	ccactgtcng	gaccaccttt	ngggagtgtt	480
ctccttacia	ccacannatg	cccggctcct	cccggaaacc	antcccancc	tgngaaggat	540
caagnctgn	atccactnnt	nctanaaccg	gccnecnccg	cngtggaacc	cnccttntgt	600
tccttttct	tnagggttaa	tnnccgcttg	gccttnccan	ngtccctnnc	nttttccnnt	660
gttnaaattg	ttangcnccc	nccnntcccn	cnnnnnnan	cccgaaccnn	annttnnann	720

ncctgggggt nccnncngat tgaccenncc nccctntant tgcnttnggg nncnntgccc 780
ctttccctct nggganncg 799

<210> 9
<211> 801
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(801)
<223> n = A,T,C or G

<400> 9
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taangatgac actcccaaag gtggctctga cagtggccca gatggacatg gggctcacct 120
caaggacaag gccaccaggt gcgggggccc aagcccacat gatccttact ctatgagcaa 180
aatccctgt gggggcttct ccttgaagtc cgccancagg gctcagtctt tggaccang 240
caggtcatgg ggttgtngnc caactggggg ccncaacgca aaanggcnaa gggcctcngn 300
caccatccc angacgcggc tacactnctg gacctcccnc tccaccactt tcatgcctg 360
ttentacccg cgnatntgtc ccantgttt cngtgccnac tccancttct nggacgtgcg 420
ctacatacgc ccggantcnc nctcccgtt tgtccctatc cacgtneccn caacaaattt 480
cncntantg caccnattec cacntttnc agntttccnc nncngcttc ctntaaaag 540
ggttganccc cggaaaatnc cccaaagggg gggggccngg tacccaactn cccctnata 600
gctgaantcc ccatnaccnn gntcnatgg anccntcctt ttaannacn tctnaactt 660
gggaananc ctcgncctn ccccnnttaa tccnccctg cnangnncnt ccccnntcc 720
ncccnntng gcntntnann cnaaaaaggc ccnnnancaa tctcctnnen cctcanttcg 780
ccanccctcg aaatcggcen c 801

<210> 10
<211> 789
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(789)
<223> n = A,T,C or G

<400> 10
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agatcctgcc ctacacactg gectccctct accaocggga gaagcaggtg ttcctgccc 180
aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttcctgc 240
caggccctaa gcctggagct ccttcccta atggacaegt ggggtgctgga ggcagtggcc 300
tgctcccacc tccaccgcg ctctggggg cctctgcctg tgatgtctcc gtacgtgtgg 360
tggtgggtga gccaccgan gocaggggtg ttcggggccg gggcatctgc ctggaoctcg 420
ccatcctgga tagtgcttcc tgctgtccca ngtggcccca tccctgttta tgggctocat 480
tgtccagctc agccagtctg tcaactgcta tatggtgtct gccgcaggcc tgggtctgg 540
ccatttact ttgtacaca ggtantattt gacaagaacg anttggccaa atactcagcg 600
ttaaaaaatt ccagcaacat tgggggtgga aggcctgcct cactgggtcc aactcccgc 660
tctgttaac ccatggggc tgccggcttg gccccaatt tctgttgctg ccaaantnat 720
gtggctctct gctgocact gttgctggct gaagtgcnta cngcncanct nggggggtng 780
ggngtccc 789

<210> 11
 <211> 772
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(772)
 <223> n = A,T,C or G

<400> 11
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 tttgttaaat aaataagtta aatattttaa tgctgtgtc tctgtgatgg caacagaagg 120
 accaacaggc cacatcctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc 180
 tgtgggctga ggggacctgg ttcttgtgtg ttgcccctca ggactcttcc cctacaaata 240
 actttcatat gttcaaatcc catggaggag tgtttcatcc tagaaactcc catgcaagag 300
 ctacattaaa cgaagctgca ggtaaggggg cttanagatg ggaaaccagg tgactgagtt 360
 tattcagctc ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc 420
 ctgagcctgg gtaatccacc tgcagagtcc ccgcattcca gtgcatggaa cccttctggc 480
 ctccctgtat aagtccagac tgaaaccccc ttggaaggnc tccagtcagg cagccctana 540
 aactggggaa aaaagaaaag gacgccccan cccccagctg tgcanctacg cacctcaaca 600
 gcacagggtg gcagcaaaaa aaccacttta ctttggcaca aacaaaaact ngggggggca 660
 accccggcac cccnangggg gttaacagga ancngggnaa cntggaaccc aattnaggca 720
 ggcccncac cccnaatntt gctgggaaat ttttctccc cttaattntt tc 772

<210> 12
 <211> 751
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(751)
 <223> n = A,T,C or G

<400> 12
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 ttggctgtgt tgggtgacgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg 180
 aagtanggtg agtcctcaaa atccgtatag ttggtgaagc cacagcactt gagccctttc 240
 atgggtggtg tccacacttg agtgaagtct tccctgggaac cataatcttt cttgatggca 300
 ggcactacca gcaacgtcag ggaagtgtc agccattgtg gtgtacacca aggcgaccac 360
 agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc 420
 acatttgctc tcagtcttan caccatanca gcccntgaaa accaananca aagaccacna 480
 cnccggctgc gatgaagaaa tnaccccneg ttgacaaact tgcatggcac tggganccac 540
 agtggccnna aaaatcttca aaaaggatgc cccatcnatt gaccccccaa atgcccactg 600
 ccaacagggg ctgcccacn cncnnaacga tganccnatt gnacaagatc tncntggtct 660
 tnatnaacnt gaaccctgcn tngtggctcc tgttcaggnc cnnngcctga cttctnaann 720
 aangaactcn gaagncccca cngganann g 751

<210> 13
 <211> 729
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(729)

<223> n = A,T,C or G

<400> 13

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tgtggancc	cagcagtncc	ctctttcaga	actcantgcc	aaganccctg	aacaggagcc	120
accatgcagt	gcttcagctt	cattaagacc	atgatgatcc	tcttcaattt	gctcatcttt	180
ctgtgtggtg	cagccctggt	ggcagtgggc	atctgggtgt	caatcgatgg	ggcctccttt	240
ctgaagatct	tccggccact	gtcgtccagt	gccatgcagt	ttgtcaacgt	gggctacttc	300
ctcatcgag	ccggcggtgt	ggtcttagct	ctaggtttcc	tgggctgcta	tgggtgctaag	360
actgagagca	agtgtgccct	cgtgacgttc	ttcttcaccc	tcctcctcat	cttcattgct	420
gaggttgcaa	tgtgtgggtc	gccttggtgt	acaccacaat	ggctgagcac	ttcctgacgt	480
tgtgtgta	gcctgccatc	aanaaaagat	tatgggttcc	caggaanact	tcactcaagt	540
gttgaacac	caccatgaaa	gggctcaagt	gctgtggctt	cnnccaacta	tacggatttt	600
gaagantcac	ctacttcaaa	gaaaaanagt	cccttccccc	atttctgttg	caattgacaa	660
acgtcccaaa	cacagccaat	tgaaaaacctg	cacccaaccc	aaanggggtcc	ccaaccanaa	720
attnaaggg						729

<210> 14

<211> 816

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(816)

<223> n = A,T,C or G

<400> 14

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tgttcgctga	aggggttgta	gtaccagcgc	gggatgctct	ccttgcagag	tcctgtgtct	120
ggcaggtcca	cgcagtggcc	tttgtcactg	gggaaatgga	tgcgctggag	ctcgtcaaa	180
ccactcgtgt	atttttcaca	ggcagcctcg	tcgcagcgtg	cggggcagtt	gggggtgtct	240
tcacactcca	ggaaactgtc	natgcagcag	ccattgctgc	agcgggaactg	ggtgggctga	300
cangtgccag	agcacactgg	atggcgccct	tccatgnnan	gggcctgng	ggaaagtccc	360
tganccocan	anctgcctct	caaangcccc	accttgcaca	ccccgacagg	ctagaatgga	420
atcttcttcc	cgaaggttag	ttnttcttgt	tgcocaaacc	anccocntaa	acaaactctt	480
gcanatctgc	tccgnggggg	tcntantacc	ancgtgggaa	aagaacccca	ggcngcgaac	540
caancttggt	tggatnccga	gcnataatct	nctnttctgc	ttggtggaca	gcaccantna	600
ctgtnnanct	ttagnccntg	gtectcntgg	gttgnncttg	aacctaatcn	ccnntcaact	660
gggacaaggt	aantngccnt	ccctttnaatt	cccnancntn	ccccctggtt	tgggggtttt	720
cncnctccta	ccocagaaan	nccgtgttcc	ccoccaacta	ggggccnaaa	ccnnttnttc	780
cacaacctn	ccccaccac	gggttcngnt	ggttng			816

<210> 15

<211> 783

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(783)

<223> n = A,T,C or G

<400> 15

ccaaggcctg	ggcaggcata	nacttgaagg	tacaacccca	ggaacccctg	gtgctgaagg	60
atgtggaaaa	cacagattgg	cgctactgc	ggggtgacac	ggatgtcagg	gtagagagga	120
aagacccaaa	ccaggtggaa	ctgtggggac	tcaaggaang	cacctacctg	ttccagctga	180
cagtgactag	ctcagaccac	ccagaggaca	cggccaacgt	cacagtcact	gtgctgtcca	240
ccaagcagac	agaagactac	tgctcgcac	ccaacaangt	gggtcgctgc	cggggctctt	300
tcccacgctg	gtactatgac	cccacggagc	agatctgcaa	gagtttcgtt	tatggaggct	360
gcttgggcaa	caagaacaac	taccttcggg	aagaagagtg	cattctancc	tgtcnggggtg	420
tgcaagggtg	gcctttgana	ngcanctctg	gggctcangc	gactttcccc	caggggccctt	480
ccatggaaaag	gcgccatcca	ntgttctctg	gcacctgtca	gccacccag	ttccgctgca	540
ncaatggctg	ctgcacnac	antttcctng	aattgtgaca	acacccccca	ntgcccccaa	600
ccctcccaac	aaagcttccc	tgttnaaaaa	tacnccantt	ggcttttnac	aaacncccg	660
cncctccntt	ttcccnntn	aaacaaagggc	nctngcnttt	gaactgcecn	aaccnnggaa	720
tctnccnngg	aaaaantncc	ccccctggtt	cctnnaancc	cctccncaaa	anctncccc	780
ccc						783

<210> 16

<211> 801

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(801)

<223> n = A,T,C or G

<400> 16

gccccaatc	cagctgccac	accacccacg	gtgactgcat	tagttcggat	gtcatataaaa	60
agctgattga	agcaaccctc	tacttttttg	tcgtgagcct	tttgcttggt	gcagggtttca	120
ttggctgtgt	tggtgacgtt	gtcattgcaa	cagaatgggg	gaaaggcact	gttctctttg	180
aagttagggtg	agtcctcaaa	atccgtatag	ttgggtgaagc	cacagcactt	gagccctttc	240
atgggtgggtg	tccacacttg	agtgaagtct	tccctgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	gaagtgtctc	gccattgtgg	tgtacaccaa	ggcgaccaca	360
gcagctgcaa	cctcagcaat	gaagatgagg	aggaggatga	agaagaacgt	cncgagggca	420
cacttgctct	ccgtcttagc	accatagcag	cccangaaac	caagagcaaa	gaccacaacg	480
ccngctgcga	atgaaagaaa	ntaccacagt	tgacaaactg	catggccact	ggacgacagt	540
tgccccgaan	atcttcagaa	aagggtatgcc	ccatcgattg	aacacccana	tgccactgc	600
cnacagggtg	gcncncncn	gaaagaatga	gccattgaag	aaggatcntc	ntgggtcttaa	660
tgaactgaaa	ccntgcatgg	tggccctgtg	tcagggtctc	tggcagtga	ttctganaaa	720
aaggaacngc	ntnagcccc	ccaaangana	aaacaccccc	gggtgttgcc	ctgaattggc	780
ggccaaggan	ccctgccccn	g				801

<210> 17

<211> 740

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(740)

<223> n = A,T,C or G

<400> 17

gtgagagcca	ggcgtccctc	tgctgccc	ctcagtggca	acacccggga	gctgttttgt	60
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cctttgtgga	gcctcagcag	ttccctcttt	cagaactcac	tgccaagagc	cctgaacagg	120
agccaccatg	cagtgttca	gcttcattaa	gaccatgatg	atcctcttca	atttgctcat	180
ctttctgtgt	ggtgcagccc	tggtggcagt	gggcatctgg	gtgtcaatcg	atggggcacc	240
ctttctgaag	atcttcgggc	cactgtcgtc	cagtgcacatg	cagtttgtca	acgtgggcta	300
cttcctcacc	gcagccggcg	ttgtgggtctt	tgctcttggt	ttcctgggct	gctatgggtc	360
taagacggag	agcaagtgtg	ccctcgtgac	gttcttcttc	atcctcctcc	tcctcttcat	420
tgctgaagtt	gcagctgctg	tggtcgcctt	gggtgacacc	acaatggctg	aaccattcct	480
gacgttgctg	gtantgctg	ccatcaanaa	agattatggg	ttcccaggaa	aaattcactc	540
aantntggaa	caccnccatg	aaaagggctc	caatttctgn	tggtttcccc	aactataccg	600
gaattttgaa	agantcncct	tacttccaaa	aaaaaanant	tgcttttnc	ccnttctgt	660
tgcaatgaaa	acntccaan	acngocaatn	aaaacctgcc	cnnncaaaaa	ggntcncaaa	720
caaaaaaant	nnaagggtn					740

<210> 18

<211> 802

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(802)

<223> n = A,T,C or G

<400> 18

ccgctgggtg	cgctgggtcca	gngnagccac	gaagcacgtc	agcatcacaca	gcctcaatca	60
caaggtcttc	cagctgccgc	acattacgca	gggcaagagc	ctccagcaac	actgcataatg	120
ggatacactt	tacttttagca	gccaggggtga	caactgagag	gtgtcgaagc	ttattcttct	180
gagcctctgt	tagtggagga	agattccggg	cttcagctaa	gtagtacagc	tatgtcccat	240
aagcaaacac	tgtgagcagc	cggaaggtag	aggcaaagtc	actctcagcc	agctctctaa	300
cattgggcat	gtccagcagt	tctccaaaca	cgtagacacc	agnggcctcc	agcacctgat	360
ggatgagtgt	ggccagcgct	gcccccttgg	ocgacttggc	taggagcaga	aattgctcct	420
ggttctgccc	tgtcaccttc	acttccgcac	tcactactgc	actgagtgtg	ggggacttgg	480
gctcaggatg	tccagagacg	tggttccgcc	ccctcnctta	atgacaccgn	ccanncaacc	540
gtcggctccc	gccgantgng	ttcgtcgtnc	ctgggtcagg	gtctgctggc	cnctacttgc	600
aancttcgtc	nggccatgg	aattcacnc	accggaactn	gtangatoca	ctnnttctat	660
aaccggnccg	caaccgnnt	ggaactccac	tcttnttnc	tttacttgag	ggtaaggtc	720
acccttncg	ttaccttgg	ccaaacctn	ccntgtgtcg	anatngtnaa	tcnggnocna	780
tnccanccnc	atangaagcc	ng				802

<210> 19

<211> 731

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(731)

<223> n = A,T,C or G

<400> 19

cnaagcttcc	aggtnacggg	ccgcnaancc	tgaccocnagg	tancanaang	cagnncngcgg	60
gagcccaocg	tcacngngng	gngtctttat	nggagggggc	ggagccacat	cnctggacnt	120
cntgaccca	actcccncc	ncncantgca	gtgatgagt	cagaactgaa	ggtnacgtgg	180
caggaacca	gancaaannc	tgctccnntc	caagtggcn	nagggggcgg	ggctggccac	240
gcncatccnt	cnagtgtgn	aaagcccn	cctgtctact	tggttgaga	acngcnnga	300

catgccccagn	gttanataac	nggcngagag	tnantttgcc	tctcccttcc	ggctgcgcan	360
cgngtntgct	tagnggacat	aacctgacta	cttaactgaa	cccngaatac	tnccnccct	420
ccactaagct	cagaacaaaa	aacttcgaca	ccactcantt	gtcacctgnc	tgctcaagta	480
aagtgtaccc	catncccaat	gtntgctnga	ngctctgncc	tgcnttangt	tcggtcctgg	540
gaagacctat	caattnaagc	tatgtttctg	actgcctctt	gtccctgna	acaancnacc	600
cnnctntcca	agggggggnc	ggccccaat	cccccaacc	ntnaattnan	tttancccn	660
ccccnggcc	cggcctttta	cnancntcnn	nnacngggna	aaaccnnngc	tttncccaac	720
nnaatccncc	t					731

<210> 20

<211> 754

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(754)

<223> n = A,T,C or G

<400> 20

tttttttttt	tttttttttt	taaaaacccc	ctccattnaa	tgnaaaacttc	cgaaattgtc	60
caacccccctc	ntccaaatnn	ccntttccgg	gnnggggttc	caaacccean	ttanntttgg	120
annttaaatt	aaatnttntt	tgngngnnna	anccnaatgt	nangaaagtt	naaccanta	180
tnancttnaa	tnccctggaaa	ccngtngntt	ccaaaaatnt	ttaaccctta	antccctccg	240
aaatngttna	nggaaaaccc	aantttctnt	aaggttggtt	gaaggntnaa	tnaaaaanccc	300
nnccaattgt	ttttngccac	gcctgaatta	attggnttcc	gntgttttcc	nttaaaaanaa	360
ggnnancccc	ggttantnaa	tccccccnnc	cccaattata	ccganttttt	ttngaattgg	420
gancccnccg	gaattaacgg	ggnnnnntccc	tnttgggggg	cnngnncccc	ccccntcggg	480
ggttngggnc	aggncnnaat	tgtttaaggg	tccgaaaaat	ccctccnaga	aaaaaanctc	540
ccaggntgag	nntnggggtt	nncccccccc	cangggccct	ctcgnaagtt	tggggtttgg	600
ggggcctggg	attttntttc	ccctnttncc	tcccccccc	ccnggganag	aggttngngt	660
tttgntcnc	ggcccccncn	aaganctttt	ccganttnan	ttaaatccnt	gcctnggcga	720
agtccnttgn	agggntaaan	ggccccctnn	cggg			754

<210> 21

<211> 755

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(755)

<223> n = A,T,C or G

<400> 21

atcancccat	gaccccnac	nnngggaccnc	tcancgggnc	nnncnaccnc	cgggccnatca	60
nngtnagnnc	actncnnttn	natacncccc	cnocnactac	gccncnanc	cnacgcncta	120
nncanatncc	actganngcg	cgangtngan	ngagaaaanct	nataccanag	ncaccanacn	180
ccagctgtcc	nanaangcct	nnnatacngg	nnnatccaat	ntgnancctc	cnaagtattn	240
nncnncan	gattttcctn	anccgattac	ccntncccc	tancccttcc	cccccaacna	300
cgaaggcnct	ggncnnaagg	nngegnncnc	ccgctagntc	cccnncnagt	cnncnnccta	360
aactcanccn	nattacncgc	ttcntgagta	tactcccccg	aatctcacc	tactcaactc	420
aaaaanactn	gatacaaaat	aatncaagcc	tgnttatnac	actntgactg	ggctctctatt	480
ttagnggtcc	ntnaancntc	ctaataactc	cagtcnccct	tcnccaattt	ccnaanggct	540
ctttcngaca	gcatnttttg	gttcccnntt	gggttcttan	ngaattgccc	ttcntngaac	600

gggctentet	tttccttcgg	ttancctggn	ttcnncgggc	cagttattat	ttcccntttt	660
aaattcntnc	cntttanttt	tggcnttcna	aaccccgggc	cttgaaaacg	gccccctggg	720
aaaaggttgt	tttganaaaa	tttttgtttt	gttcc			755

<210> 22

<211> 849

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(849)

<223> n = A,T,C or G

<400> 22

tttttttttt	tttttangtg	tngtcgtgca	ggtagaggct	tactacaant	gtgaanacgt	60
acgctnngan	taangcgacc	cgantttctag	ganncnccct	aaaatcanac	tgtgaagatn	120
atcctgnnna	cggaanggtc	accggnggat	nntgctaggg	tgncenctcc	cannncnttn	180
cataactcng	nggcccctgcc	caccaccttc	ggcgggcccg	ngnccggggc	cggggtcattn	240
gnnttaaccn	cactnngcna	ncggtttccn	ncccnncng	accngggcga	tccgggggtnc	300
tctgtcttcc	cctgnagncn	anaaantggg	ccnccggnccc	ctttacccct	nnacaagcca	360
cngccntcta	ncenengccc	cccctccant	nngggggact	gcnannngct	ccgttntctng	420
nnaccccnnn	gggtncctcg	gttgtcgant	cnaccgnang	ccanggatcc	cnaaggaagg	480
tgcgttnttg	gccccctacc	ttcgctncgg	nncacccttc	ccgaananga	ncegctcccc	540
cnenncgng	cctcncctcg	caacacccgc	ntctcngt	ncggnnnccc	ccccacccgc	600
ncctcncnc	ngnccgnancn	ctccnccncc	gtctcannca	ccaccccgcc	ccgccaggcc	660
ntcanccacn	ggngaenng	nagcncnttc	gcncgcgcgn	gcgnccctcc	cgccnccngaa	720
ctnctcngg	ccantnnccg	tcaanccnna	cnaaacgcgc	ctgcgcggcc	cgncgcgncc	780
ncctcncga	gtcctccccn	cttccnacc	angnnttcn	cgaggacacn	nnaccccgcc	840
nncangcgg						849

<210> 23

<211> 872

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(872)

<223> n = A,T,C or G

<400> 23

gcgcaaaacta	tacttcgctc	gnactcgtgc	gcctcgcctnc	tcttttctctc	cgcaaccatg	60
tctgacnanc	ccgattnggc	ngatatcnan	aagntcganc	agtccaaact	gantaaacaca	120
cacacnncan	aganaaatcc	netgccttcc	anagtanacn	attgaacnng	agaaoacangc	180
nggcgaatcg	taatnaggcg	tgcgcgcgca	atntgtcncc	gtttattntn	ccagctctcnc	240
ctnccnacc	tactctctcn	nagctgtcnn	acccctngtn	cgnacccccc	naggctcgga	300
tcgggtttnn	nntgaocgng	cnnoecctcc	ccocntccat	naaganccnc	ccgcaccacc	360
nanngcncgc	ncoccgnnct	cttegcnccc	ctgtcctntn	cccctgtngc	ctggcnengn	420
accgcattga	ccctcgccnn	ctncnngaaa	ncgnanacgt	ccgggttggn	annanogctg	480
tgggnnnngcg	tctgcncgc	gttctctccn	ncnncttoca	ccatcttctt	taennggtct	540
ccnccgcttc	tcnnncaacn	cctgggaagc	tntcctntgc	cccccttnac	ccccccctt	600
cgncgtgncc	cgnccccacc	ntcatttnca	naegntcttc	acaannncc	ggntnnctcc	660
cnancngnncn	gtcanccnag	ggaagggngg	ggnnccnntg	nttgacgttg	ngngangtc	720
cgaanantcc	tcnccntcan	cnetacccct	egggcggnct	ctcngttnc	aacttancaa	780

ntctcccccg ngngcnctc tcagcctcnc cncnccnct ctctgcantg tntctgtctc 840
tnaccnntac gantnttcgn cncctcttcc cc 872

<210> 24
<211> 815
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(815)
<223> n = A,T,C or G

<400> 24
gcatgcaagc ttgagtattc tatagngtca cctaaatanc ttggcntaat catggtcnta 60
nctgncttcc tgtgtcaaat gtatacnaaa tanatatgaa tctnatntga caagannnga 120
tcntncatta gtaacaantg tnttgtccat cctgtcngan canattccca tnnattncgn 180
cgcattcnen gencantatn taatngggaa ntcnnntnnn ncaccnncat ctatcntncc 240
gcncctgac tggagagat ggatnanttc tntntgacc nacatgttca tcttggattn 300
aanancccc cgcngnccac cggttngnng cnagecnntc ccaagacctc ctgtggagggt 360
aacctgcgtc aganncatca aacntgggaa acccgcncc angtnnaagt ngnnncanan 420
gatccccgtc agnttnnacc atcccttcnc agcgcacct ttngtgcctt anagnnagc 480
gtgtccnanc cnetcaacat ganacgcgcc agnccanccg caattnggca caatgtcgnc 540
gaaccccccta gggggantna tncaaanccc caggattgtc cncncangaa atcccnanc 600
ccnccctac cennctttgg gacngtgacc aantcccga gtncagtc ggcngnctc 660
ccccaccggt nncntgggg ggggaanct cngnntcanc cngncgaggn ntcgnaagga 720
accggnctn ggncgaanng ancnntcnga agngccnct cgtataacce cccctcncca 780
nccnacngnt agntcccccc cngggtnccg aangg 815

<210> 25
<211> 775
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(775)
<223> n = A,T,C or G

<400> 25
ccgagatgtc tcgctccgtg gccttagctg tgctcgcgct actctctctt tctggcctgg 60
aggctatcca gcgtactcca aagattcagg ttactcacg tcatccagca gagaatggaa 120
agtcaaattt cctgaattgc tatgtgtctg ggtttcatcc atccgacatt gaanttgaact 180
tactgaagaa tgganagaga attgaaaaag tggagcattc agacttgtct ttcagcaagg 240
actgggtctt ctatctctng tactacactg aattcacccc cactgaaaaa gatgagtatg 300
cctgccgtgt gaaccatgtg actttgtcac agcccaagat agttaagtgg gatcgagaca 360
tgtaagcagn cncatggaa gtttgaagat gccgcatttg gattggatga attccaaatt 420
ctgcttgctt gcnttttaat antgatatgc ntatacacc taccctttat gnccccaaat 480
tgtaggggtt acatnantgt tcnctnngga catgatcttc ctttataant cncncttcg 540
aattgcccgt cncnngttn ngaatgttcc cnaaaccacg gttggctccc ccaggtncc 600
tcttacggaa gggcctgggc cnccttncaa ggttggggga accnaaaatt tcncttntgc 660
cncnccncca cnccttgng nncncanttt ggaacccttc cnattccctc tggcctcnna 720
nccttnncta anaaaacttn aaancgtngc naaanntttn acttcccccc ttacc 775

<210> 26

<211> 820

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(820)

<223> n = A,T,C or G

<400> 26

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anattantac agtgtaatct tttcccagag gtgtgtanag ggaacggggc ctagaggcat      60
cccanagata ncttatanca acagtgcctt gaccaagagc tgctgggcac atttcctgca      120
gaaaagggtg cgggtcccat cactectect ctcccatagc catcccagag gggtagtag      180
ccatcangcc ttcgggtggga gggagtcang gaaacaacan accacagagc anacagacca      240
ntgatgaaca tgggcgggag cgagcctctt ccctgnaccg ggggtggcana nganagccta      300
nctgaggggt cacactataa acgttaacga ccnagatnan cacctgcttc aagtgcaccc      360
ttcttaacct acnaccagn accnnnaact gcngcctggg gacagcncct ggancagcta      420
acnnagcact cacctgcccc cccatggccg tncgctctcc tggtcctgnc aagggaagct      480
ccctgttgga attncgggga naccaaggga nccccctcc ccanctgtga aggaaaaann      540
gatggaattt tnccttccg gccnntcccc tcttcttta cagccccct nntactctc      600
tccctctntt ntectgnenc acttttnacc ccnnnatttc ccttnattga tcggannctn      660
ganattccac tnnccctnc cntcnatcg naanacnaaa nactntctna cccnggggat      720
gggnnccctg ntcatectct ctttttctc accnccnntt ctttgcctct ccttngatca
780tccaacntc gntggccntn ccccccnntt tcttttcccc
820

```

<210> 27

<211> 818

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(818)

<223> n = A,T,C or G

<400> 27

```

tctgggtgat ggctcttcc tctcagggga cctctgactg ctctgggoca aagaatctct      60
tgtttcttct ccgagcccca ggcagcgggtg attcagocct gcccaaocctg attctgatga      120
ctgcggatgc tgtgaaggac ccaaggggca aatagggtcc cagggtocag ggagggggcg      180
ctgctgagca ctcccgcccc tcaocctgcc cagccctgc catgagctct gggctgggtc      240
tccgcctcca ggggtctgct cttccangca ngccancaag tggcgctggg ccacactggc      300
ttcttctgct cccntcctg gctctgantc tctgtcttcc tgctctgtgc angcnccttg      360
gatctcagtt tccctcncctc anngaactct gttctgann tcttcantta actntgantt      420
tatnaccnan tggnetgtnc tgcnnactt taatgggocn gaccggctaa tccctccctc      480
nctoccttcc anttcnnnna accngcttnc cntctctcc ccntancccg ccnggggaanc      540
ctcctttgcc ctnaaccang gccnnnaocg ccctnnctn ggggggcnng gttnctnenc      600
ctgntnccc cnetcnnt tncctgtcc cnnccnccn nngcannttc ncngtcccn      660
tnnctcttcn ngntcgnaa ngntcnctn tnnnnngcn ngntnntn tccctctcnc      720
cnnntgnang tnnntnnnc ncnngncccc nnnnccnnnn nggnntnnn tctnncngc      780
cccncccc ngnattaagg cctcnnctc ccggccnc      818

```

<210> 28

<211> 731

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(731)

<223> n = A,T,C or G

<400> 28

aggaagggcg	gagggatatt	gtanggggatt	gagggatagg	agnataangg	gggaggtgtg	60
tcccaacatg	anggtgnngt	tctcttttga	angaggggtg	ngtttttann	ccnggtgggt	120
gattnaaccc	cattgtatgg	agnnaaaggn	tttnagggat	tttctggctc	ttatcagtat	180
ntanattcct	gtnaatcgga	aaatnatntt	tcnncnggaa	aatnttgctc	ccatccgnaa	240
attinctccg	ggtagtgc	ntingggggg	cngccangtt	tcccaggctg	ctanaatcgt	300
actaaagntt	naagtgggan	tncaaataaa	aacctnnac	agagnatccn	tacccgactg	360
tnnnntncct	tcgcccctng	actctgcng	agcccaatac	ccnngngnat	gtcncncngn	420
nnngcgnnc	tgaaannnnc	tcgnggctnn	gancatcang	gggtttcgca	tcaaaagcnn	480
cgtttcncat	naaggcactt	tngcctcatc	caaccnctng	ccctcnncca	tttngccgctc	540
nggttcncct	acgctnnntg	cncctnnntn	ganattttnc	ccgcttnggg	naancctcct	600
gnaatgggta	gggncttntc	ttttnacenn	gnggtntact	aatcnnctnc	acgcntnctt	660
tctcnacccc	ccccctttt	caatcccanc	ggcnaatggg	gtctcccn	cgangggggg	720
nnnccannnc	c					731

<210> 29

<211> 822

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(822)

<223> n = A,T,C or G

<400> 29

actagtccag	tgtggtggaa	ttccattgtg	ttggggncnc	ttctatgant	antnttagat	60
cgtctanacc	tcacancctc	ccnacnangc	ctataangaa	nannaataga	netgtncnnt	120
atntntacnc	tcatanncct	cnnnaccac	tcctcttaa	cccctactgt	gcctatngcn	180
tnnctantct	ntgccgcctn	cnanccaccn	gtgggcnac	cncnngnat	ctcnatctcc	240
tcnccatntn	gcctananta	ngtncatacc	ctatacctac	nccaatgcta	nnnctaancn	300
tccatnantt	annntaacta	ccactgacnt	ngactttcnc	atnancctct	aatttgaatc	360
tactctgact	cccacngcct	annnattagc	ancntcccc	nacnatntct	caaccaaatc	420
ntcaacaacc	tatctanctg	ttcnccaacc	nttnccctcg	atccccnnac	aacccccctc	480
ccaaataccc	nccacctgac	ncctaaccen	caccatcccg	gcaagccnan	ggncatttan	540
ccactggaat	cacnatngga	naaaaaaac	ccnaactctc	tancncnnat	ctccctaana	600
aatnctcctn	naatttactn	ncantnccat	caancccaen	tgaaaacnnaa	ccccgtttt	660
tanatccctt	ctttcgaaaa	ccnacccttt	annncccaac	ctttngggcc	ccccnctnc	720
ccnaatgaag	gncncccaat	cnangaaacg	nccntgaaaa	ancnaggcna	anannntccg	780
canatccctat	cccttanttn	ggggncctt	nccnngggcc	cc		822

<210> 30

<211> 787

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(787)

<223> n = A,T,C or G

<400> 30

cgccgcctg	ctctggcaca	tgcctcctga	atggcatcaa	aagtgatgga	ctgcccattg	60
ctagagaaga	ccttctctcc	tactgtcatt	atggagccct	gcagactgag	ggctccccct	120
gtctgcagga	tttgatgtct	gaagtcgtgg	agtgtggctt	ggagctcctc	atctacatna	180
gctggaagcc	ctggaggggc	tctctcgcca	gcctccccct	tctctccacg	ctctccangg	240
acaccagggg	ctccaggcag	cccattattc	ccagnangac	atgggtgttc	tccacgcgga	300
cccatggggc	ctgnaaggcc	agggtctcct	ttgacaccat	ctctcccgtc	ctgcttggca	360
ggccgtggga	tccactantt	ctanaacggg	cgccaccncc	gtgggagctc	cagcttttgt	420
tcccnttaat	gaaggttaat	tgcncgcttg	gcgtaatcat	nggtcanaac	tntttcctgt	480
gtgaaattgt	ttntccccct	ncnattccnc	ncnacatacn	aacccgggan	cataaagtgt	540
taaagcctgg	gggtngcctn	nngaataaac	tnaactcaat	taattgcgtt	ggctcatggc	600
ccgctttccn	ttcnggaaaa	ctgtcntccc	ctgcnttntt	gaatcggcca	ccccccnggg	660
aaaagcgggt	tgcnttttng	ggggntcctt	ccncttcocc	cctcnctaan	ccctncgcct	720
cggtcgttnc	nggtngcggg	gaanggggat	nnnctccccc	naagggggng	agnnnngtat	780
ccccaaa						787

<210> 31

<211> 799

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(799)

<223> n = A,T,C or G

<400> 31

tttttttttt	tttttttggc	gatgctactg	tttaattgca	ggaggtgggg	gtgtgtgtac	60
catgtaccag	ggctattaga	agcaagaagg	aaggaggagg	ggcagagcgc	cctgctgagc	120
aacaaaggac	tcctgcagcc	ttctctgtct	gtctcttggc	gcaggcacat	ggggaggcct	180
cccgacgggt	ggggggccacc	agtocagggg	tgggagcact	acanggggtg	ggagtgggtg	240
gtggctggtg	cnaatggcct	gncacanatc	cctacgatcc	ttgacacctg	gatttcacca	300
ggggaccttc	tgttctccca	nggnaacttc	ntnnatctcn	aaagaacaca	actgtttcct	360
cngcanttct	ggctgttcat	ggaaagcaca	ggtgtccnat	ttnggctggg	acttgggtaca	420
tatggttccg	gcccacctct	cccntcnaaa	aagtaattca	ccccccccc	ccntctnttg	480
cctgggocct	taantaacca	caecggaact	canttantta	ttcatcttng	gntgggcttg	540
ntnatcncn	cctgaangcg	ccaagttgaa	aggccacgcc	gtncocnctc	cccatagnan	600
ntttttnnct	canctaattg	ccccccnggc	aacnatocaa	ttccccccc	tgggggcccc	660
agcccanggc	ccccgnetcg	ggnnnccngn	cncgnantcc	ccaggntctc	ccantcngnc	720
ccnnngcncc	cccgacgcga	gaacanaagg	ntngagccnc	cgcannnnnn	nggtnnnnc	780
ctcgccccc	ccnncgng					799

<210> 32

<211> 789

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(789)

<223> n = A,T,C or G

<400> 32

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tttttccnag	ggcagggttta	ttgacaacct	cncgggacac	aancaggctg	gggacaggac	120
ggcaacaggc	tccggcgggc	gcggcgggcg	ccctacctgc	ggtaccaaat	ntgcagcctc	180
cgctcccgt	tgatnttcct	ctgcagctgc	aggatgccnt	aaaacagggc	ctcggccntn	240
ggtgggcacc	ctgggatttn	aatttccacg	ggcacaatgc	ggtcgcancc	cctcaccacc	300
nattaggaat	agtggtnnta	cccncncncg	ttggcncact	ccccntggaa	accacttntc	360
gcggctccgg	catctgggtc	taaaccttgc	aaacnctggg	gccctctttt	tggttantnt	420
nccngccaca	atcatnactc	agactggcnc	gggctggccc	caaaaaancn	ccccaaaacc	480
ggnccatgtc	ttnnccgggt	tgctgcnatn	tncatcacct	cccgggcnca	ncaggncaac	540
ccaaaagtcc	ttgnngcccn	caaaaaanct	ccggggggnc	ccagtttcaa	caaagtcac	600
ccccttgccc	cccaaatact	ccccccgntt	netgggtttg	ggaacccacg	cctctnnctt	660
tggnnggcaa	gntggntccc	ccttcggggc	cccgggtggg	ccnntcttaa	ngaaaacncc	720
ntcctnnnca	ccatcccccc	nngnnacgnc	tancaangna	tecctttttt	tanaaacggg	780
ccccccnccg						789

<210> 33

<211> 793

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(793)

<223> n = A,T,C or G

<400> 33

gacagaacat	gttggatggg	ggagcacctt	tctatacgac	ttacaggaca	gcagatgggg	60
aattcatggc	tggtggagca	atanaacccc	agttctacga	gctgctgac	aaaggacttg	120
gactaaagtc	tgatgaactt	cccaatcaga	tgagcatgga	tgattggcca	gaaatgaana	180
agaagtttgc	agatgtatnt	gcaaagaaga	cgaaggcaga	gtgggtgtcaa	atctttgacg	240
gcacagatgc	ctgtgtgact	ccggttctga	cttttgagga	ggttgttcat	catgatcaca	300
acaangaacg	gggctcggtt	atcaccantg	aggagcagga	cgtgagcccc	cgccctgcac	360
ctctgctggt	aaacacccca	gccatccctt	ctttcaaaag	ggatccacta	cttctagagc	420
ggncgcacc	gcgggtggagc	tccagctttt	gttcccttta	gtgagggtta	attgcgcgct	480
tggcgtaatc	atggtcatan	ctgtttcctg	tgtgaaattg	ttatccgctc	acaattccac	540
acaacatacg	anccggaagc	atnaaatttt	aaagcctggg	ggtngcctaa	tgantgaact	600
nactcacatt	aattggcttt	gcgctcactg	cccgttttcc	agtcgggaaa	acctgtcctt	660
gccagctgcc	nttaatgaat	cnggccaccc	cccggggaaa	aggcngtttg	cttnttgggg	720
cgcncttccc	gctttctcgc	ttcctgaant	ccttcccccc	ggtctttcgg	cttgcggcna	780
acggtatcna	cct					793

<210> 34

<211> 756

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(756)

<223> n = A,T,C or G

<400> 34

gccgcgaccg	gcattgtacga	gcaactcaag	ggcgagtggg	accgtaaaag	ccccaatctt	60
ancaagtgcg	gggaanagct	gggtcgactc	aagctagtgc	ttctggagct	caacttcttg	120

ccaaccacag	ggaccaagct	gaccaaacag	cagctaattc	tggcccggtga	catactggag	180
atcgggggccc	aatggagcat	cctacgcaan	gacatcccct	ccttcgagcg	ctacatggcc	240
cagctcaaat	gctactactt	tgattacaan	gagcagctcc	ccgagtcagc	ctatatgcac	300
cagctcttgg	gcctcaacct	cctcttcttg	ctgtcccaga	accgggtggc	tgantnccac	360
acgganttgg	ancggctgcc	tgcccaanga	catacanacc	aatgtctaca	tcnaccacca	420
gtgtcctgga	gcaatactga	tggangggcag	ctaccncaaa	gtnttcctgg	ccnagggtaa	480
catccccgcg	cgagagctac	accttcttca	ttgacatcct	gctcgacact	atcagggatg	540
aaaatcgcn	ggttgctcca	gaaaggctnc	aanaanatcc	ttttcnctga	aggcccccg	600
atncnctagt	nctagaatcg	gcccgccatc	gcgggtgganc	ctccaaacct	tcgttncct	660
ttactgaggg	ttnattgccg	cccttggcgt	tatcatggtc	acncngttn	cctgtgttga	720
aattnttaac	ccccacaaat	tccacgccna	catting			756

<210> 35

<211> 834

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(834)

<223> n = A,T,C or G

<400> 35

ggggatctct	anactnacct	gnatgcatgg	ttgtcgggtg	ggtcgctgtc	gatgaanatc	60
aacaggatct	tgccttgaa	gctctcggt	gctgtnttta	agttgctcag	tctgccgtca	120
tagtcagaca	cnccttggg	caaaaaacan	caggatntga	gtcttgattt	cacctccaat	180
aatcttcngg	gctgtctgt	cggtgaactc	gatgacnang	ggcagctggg	tgtgtntgat	240
aaantccanc	angttctct	tggtgacctc	cccttcaaag	ttgttcgggc	cttcatcaaa	300
cttctnnaan	angannancc	canctttgtc	gagctggnat	ttgganaaca	cgtaacctgt	360
ggaaactgat	cccaaagtgt	atgtcatcca	tgcctctgtc	tgcctgcaaa	aaacttgctt	420
ggcncaaacc	cgactcccn	tccttgaaa	aagccnatca	cacccccctc	cctggactcc	480
nncaangact	ctnccgctnc	ccntccnng	cagggttggg	ggcannccgg	gcccntgcgc	540
ttcttcagcc	agttcacnat	nttcattcagc	ccctctgcca	gctgtnttat	tccttggggg	600
ggaanccgtc	tctcccttcc	tgaannaact	ttgaccgtng	gaatagccgc	gentcnccnt	660
acntnctggg	ccgggttcaa	antccctccn	ttgncnntcn	cctcgggcca	ttctggattt	720
nccnaacttt	ttccttcccc	cncnccnccg	ngtttggntt	tttcatnggg	ccccaaactc	780
gctnttggcc	antccctggg	gggcntntan	cncnccntnt	ggtcnccntng	ggcc	834

<210> 36

<211> 814

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(814)

<223> n = A,T,C or G

<400> 36

cggnccgttt	cncgccgcgc	cccggttcca	tgacnaaggc	tccttcang	ttaaatacnn	60
cctagnaaac	attaatgggt	tgtctactta	atacatcata	cnaaacagta	agcctgccca	120
naacgccaac	tcaggccatt	cctaocaaag	gaagaaaggc	tggtctctcc	acccccgtga	180
ggaaaggcct	gccttgtaag	acaocacaat	ncggctgaat	ctnaagtctt	gtgttttact	240
aatggaaaaa	aaaaataaac	aanagggttt	gttctcatgg	ctgccaccgc	cagcctggca	300
ctaaaacanc	ccagcgctca	cttctgcttg	ganaaatatt	ctttgctctt	ttggacatca	360

ggcttgatgg	tatcactgcc	acntttccac	ccagctgggc	ncccttcccc	catntttgtc	420
antganctgg	aaggcctgaa	ncttagtctc	caaaagtctc	ngcccacaag	accggccacc	480
aggggangtc	ntttncagtg	gatctgccaa	anantaccn	tatcatcnnt	gaataaaaag	540
gcccctgaac	ganatgcttc	cancancctt	taagaccat	aatcctngaa	ccatgggtgcc	600
cttccggtct	gatacnaaag	gaatgttcct	gggtcccant	ccctcctttg	tttcttacgt	660
tgtnttgga	cctgctngn	atnaccnaan	tganatcccc	ngaagcacc	tnccctggc	720
atttganttt	cntaaattct	ctgccctacn	nctgaaagca	cnattccctn	ggcnccnaan	780
ggngaactca	agaaggtctn	ngaaaaacca	cncn			814

<210> 37

<211> 760

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(760)

<223> n = A,T,C or G

<400> 37

gcatgctgct	cttcctcaaa	gttgttcttg	ttgccataac	aaccaccata	ggtaaagcgg	60
gcgcagtgtt	cgtggaaggg	gttgtagtac	cagcgcgga	tgctctcctt	gcagagtcct	120
gtgtctggca	gggtccacgca	atgccctttg	tcactgggga	aatggatgcg	ctggagctcg	180
tcnaanccac	tcgtgtattt	ttcacangca	gcctcctcgg	aagctccggg	gcagttgggg	240
gtgtcgtcac	actccactaa	actgtcgatn	cancagccca	ttgtgcagc	ggaactgggt	300
gggctgacag	gtgccagaac	acactggatn	ggcctttcca	tggaagggcc	tgggggaaat	360
cncctnanc	caaactgcct	ctcaaaggcc	accttgccca	ccccgacagg	ctagaaatgc	420
actcttcttc	ccaaaggtag	ttgttcttgt	tgcccaagca	ncctccanca	aaccaaaanc	480
ttgcaaaatc	tgtcccggtg	gggtcatnnn	taccanggtt	ggggaaanaa	accggcgngn	540
ganccnctt	gtttgaatgc	naaggnaata	atcctcctgt	cttgcttggg	tggaanagca	600
caattgaact	gttaacnttg	ggccgngttc	cnctnggggtg	gtctgaaact	aatcaccgtc	660
actggaaaaa	ggtangtgcc	ttccttgaat	tcccaaantt	ccccngntt	tgggtntttt	720
ctcctctncc	ctaaaaatcg	tnttcccccc	cntanggcg			760

<210> 38

<211> 724

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(724)

<223> n = A,T,C or G

<400> 38

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cttccnaaat	tgccaacccc	cctcnnccaa	atnnccattt	ccgggggggg	gttccaaacc	120
caaattaatt	ttgganttta	aattaaatnt	tnattngggg	aanaanccaa	atgtnaagaa	180
aatttaaccc	attatnaact	taaatncctn	gaaaccctng	gnttccaaaa	atttttaacc	240
cttaaatccc	tccgaaattg	ntaanggaaa	accaaattcn	cctaaggctn	tttgaaggtt	300
ngatttaaac	ccccttnant	tnttttnacc	cnngnctnaa	ntatttngnt	tccggtgttt	360
tcctnttaan	cnntngtaac	tcccgnataat	gaannnccct	aanccaatta	aaccgaattt	420
tttttgaatt	ggaaattccn	ngggaattna	ccgggggttt	tcccttttgg	gggccatncc	480
cccnctttcg	gggtttgggn	ntaggttgaa	tttttnnang	ncccaaaaaa	ncccccaana	540
aaaaaactcc	caagnnttaa	ttngaattnc	ccccctccca	ggccttttgg	gaaagngggg	600

tttntggggg	ccngggantt	cnttccccn	ttncncccc	ccccccnggt	aaanggttat	660
ngnntttggt	ttttgggccc	cttnanggac	cttccggatn	gaaattaaat	ccccgggneg	720
gccg						724

<210> 39

<211> 751

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(751)

<223> n = A,T,C or G

<400> 39

tttttttttt	tttttctttg	ctcacattta	atttttattt	tgattttttt	taatgctgca	60
caacacaata	tttatttcat	ttgtttcttt	tatttcat	tatttggttg	ctgctgctgt	120
tttatttatt	tttactgaaa	gtgagagggg	acttttgtgg	ccttttttcc	tttttctgta	180
ggccgcctta	agctttctaa	atttggaa	tctaagcaag	ctgaanggaa	aaggggggtt	240
cgcaaaatca	ctcgggggaa	nggaaaggtt	gctttgttaa	tcatgcccta	tggtgggtga	300
ttaactgctt	gtacaattac	ntttcacttt	taattaattg	tgctnaangc	tttaattana	360
cttggggggt	ccctccccc	accaacccc	ctgacaaaa	gtgccngccc	tcaaattnatg	420
tcccggnnt	cnttgaaaca	cacngcngaa	ngttctcatt	ntcccccnc	caggtnaaaa	480
tgaaggggta	ccatntttta	cncacctcc	acntggcnnn	gcctgaatcc	tcnaaaancn	540
ccctcaancn	aattnctnng	ccccggtcnc	gentnngtc	cncgggggt	ccgggaantn	600
cacccccnga	anncnntnnc	naacnaaatt	ccgaaaatat	tcccnntcnc	tcaattcccc	660
cnnagactnt	cctcnnncn	cncaattttc	ttttnttcac	gaacncgnnc	cnaaaatgn	720
nnnnncctc	cncnngtcn	naatcnccan	c			751

<210> 40

<211> 753

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(753)

<223> n = A,T,C or G

<400> 40

gtgggtatttt	ctgtaagatc	aggtgttcct	ccctogtagg	tttagaggaa	acaocctcat	60
agatgaaaac	ccccccgaga	cagcagcact	gcaactgoca	agcagccggg	gtaggagggg	120
cgccctatgc	acagctgggc	ccttgagaca	gcagggtctc	gatgtcaggc	tcgatgtcaa	180
tggtctggaa	gcggcggtg	tacctgcgta	ggggcacacc	gtcaggggcc	accaggaact	240
tctcaaagtt	ccaggcaacn	tcgttgcgac	acaccggaga	ccagggtgatn	agcttgggggt	300
cggtcataan	cgcggtggcg	tcgtcgtggt	gagctggcag	ggocctccgc	aggaaggcna	360
ataaaaggtg	cgccccgcga	ccgttcant	cgcacttctc	naanaocatg	angttgggct	420
cnaaccacc	accannccgg	acttccctga	nggaattccc	aatctctctc	gntcttgggc	480
ttctnctgat	gcccctantg	gttgcccnng	atgccaanca	nccccaancc	ccgggggtcct	540
aaanacccn	cctoctcntt	tcattctgggt	tnntntcccc	ggaccntggg	tcctctcaag	600
ggancccata	tctcnaccan	tactcaccnt	nccccccent	gnnaccanc	cttctannng	660
ttccncccg	ncctctggcc	cntcaaan	gcttncaena	cctgggtctg	ccttcccccc	720
tnccctatct	gnaocccn	ttgtctcan	tn			753

<210> 41

<211> 341
 <212> DNA
 <213> Homo sapien

<400> 41
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 agtgaaccca tcttgattt atatacatat atgttctcag tattttggga gcctttccac 120
 ttctttaaac ctgttcatt atgaacactg aaaataggaa tttgtgaaga gttaaaaagt 180
 tatagcttgt ttacgtagta agtttttgaa gtctacattc aatccagaca cttagttgag 240
 tgttaaactg tgatttttaa aaaatatcat ttgagaatat tctttcagag gtattttcat 300
 ttttactttt tgattaattg tgttttatat attagggtag t 341

<210> 42
 <211> 101
 <212> DNA
 <213> Homo sapien

<400> 42
 acttactgaa tttagtctg tgctcttctt tatttagtgt tgtatcataa atactttgat 60
 gtttcaaaca ttctaataa ataattttca gtggcttcat a 101

<210> 43
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 43
 acatctttgt tacagtctaa gatgtgttct taaatcacca ttcttctctg gtcttcaccc 60
 tccagggtgg tctcacactg taattagagc tattgaggag tctttacagc aaattaagat 120
 tcagatgcct tgctaagtct agagttctag agttatgttt cagaaagtct aagaaaccca 180
 cctcttgaga ggtcagtaaa gaggacttaa tatttcatat ctacaaaatg accacaggat 240
 tggatacaga acgagagtta tcttgataa ctcagagctg agtacctgcc cgggggcccgc 300
 tcgaa 305

<210> 44
 <211> 852
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (852)
 <223> n = A,T,C or G

<400> 44
 acataaatat cagagaaaag tagtctttga aatatttacg tccaggagtt ctttgtttct 60
 gattatttgg tgtgtgtttt gggttgtgtc caaagtattg gcagcttcag ttttcatttt 120
 ctctccatcc tcgggcattc ttcccaaatt tatataccag tcttcgtcca tccacacgct 180
 ccagaatttc tctttttag taatatctca tagctcggct gagcttttca taggtcatgc 240
 tgctgttgtt cttcttttta cccatagct gagccactgc ctctgatttc aagaacctga 300
 agacgccctc agatcggctc tcccatttta ttaatcctgg gttcttgtct gggttcaaga 360
 ggatgtcgcg gatgaattcc cataagttag tccctctcgg gttgtgcttt ttgggtgtggc 420
 acttggcagg ggggtcttgc tcctttttca tatcagggtga ctctgcaaca ggaaggtgac 480
 tgggtggtgt catggagatc tgagcccggc agaaagtttt gctgtccaac aaatctactg 540
 tgctaccata gttggtgtca tataaatagt tctngtcttt ccagggtgtc atgatggaag 600

gctcagtttg	ttcagtcctg	acaatgacat	tgtgtgtgga	ctggaacagg	tcactactgc	660
actggccggt	ccacttcaga	tgctgcaagt	tgctgtagag	gagntgcccc	gccgtccctg	720
ccgccccggg	gaactcctgc	aaactcatgc	tgcaaagggt	ctcgccgttg	atgtcgaact	780
cntggaaagg	gatacaattg	gcatacagct	ggttgggtgtc	caggagggtga	tggagccact	840
cccacacctg	gt					852

<210> 45

<211> 234

<212> DNA

<213> Homo sapien

<400> 45

acaacagacc	cttgctcgct	aacgacctca	tgctcatcaa	gttggacgaa	tccgtgtccg	60
agtctgacac	catccggagc	atcagcattg	cttcgcagtg	ccctaccgcg	gggaactctt	120
gcctcgtttc	tggctggggg	ctgctggcga	acggcagaat	gcctaccgtg	ctgcagtgcg	180
tgaacgtgtc	ggtgggtgtc	gaggagggtc	gcagtaagct	ctatgacccg	ctgt	234

<210> 46

<211> 590

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(590)

<223> n = A,T,C or G

<400> 46

actttttatt	taaatgttta	taaggcagat	ctatgagaat	gatagaaaac	atgggtgtgta	60
atttgatagc	aatatttttg	agattacaga	gttttagtaa	ttaccaatta	cacagttaaa	120
aagaagataa	tatattccaa	gcanatacaa	aatatcta	gaaagatcaa	ggcaggaaaa	180
tgantataac	taattgacaa	tggaaaaatca	attttaatgt	gaattgcaca	ttatoccttta	240
aaagctttca	aaanaaanaa	ttattgcagt	ctanttaatt	caaacagtgt	taaatgggtat	300
caggataaan	aactgaaggg	canaaaagaat	taattttcac	ttcatgtaac	ncacccanat	360
ttacaatggc	ttaaatgcan	ggaaaaagca	gtggaagtag	ggaagtantc	aaggtctttc	420
tggctctctaa	tctgccttac	tcttgggtg	tggctttgat	cctctggaga	cagctgccag	480
ggctcctggt	atatccacaa	tcccagcagc	aagatgaagg	gatgaaaaag	gacacatgct	540
gccttctctt	gaggagactt	catctcactg	gccaacactc	agtcacatgt		590

<210> 47

<211> 774

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(774)

<223> n = A,T,C or G

<400> 47

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tgaacagaat	tttctgnac	aaoggggctt	caaaaataatt	ttcttgggga	ggttcaagac	120
gcttcactgc	ttgaaactta	aatggatgtg	ggacanaatt	ttctgtaatg	acctgagggg	180
cattacagac	gggactctgg	gaggaaggat	aaacagaaag	gggacaaagg	ctaatcccaa	240
aacatcaaag	aaaggaagggt	ggcgtcatat	ctcccagcct	acacagtctt	ccagggtctt	300

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cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctctgtgtg 360
ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgctgat cctgcgtggc 420
ccacactcct tgaacacaca tccccaggtt atattcctgg acatggctga acctcctatt 480
cctacttccg agatgccttg ctccctgcag cctgtcaaaa tcccactcac cctccaaacc 540
acggcatggg aagcctttct gacttgcttg attactccag catcttgga caatccctga 600
ttccccactc cttagaggca agatagggtg gttaagagta gggctggacc acttgagacc 660
aggctgctgg cttcaaattn tggctcattt acgagctatg ggaccttggg caagtnatct 720
tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt 774

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<210> 48
<211> 124
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(124)
<223> n = A,T,C or G

```

```

<400> 48
canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt 60
ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact 120
tggt 124

```

```

<210> 49
<211> 147
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(147)
<223> n = A,T,C or G

```

```

<400> 49
gccgatgcta ctattttatt gcaggagggtg ggggtgtttt tattattctc tcaacagctt 60
tgtggctaca ggtgggtgtct gactgcatna aaaanttttt tacgggtgat tgcaaaaatt 120
ttagggcacc catatcccaa gcantgt 147

```

```

<210> 50
<211> 107
<212> DNA
<213> Homo sapien

```

```

<400> 50
acattaaatt aataaaaagga ctgttggggt tctgctaaaa cacatggctt gatataattgc 60
atggtttgag gttaggagga gttaggcata tgttttggga gaggggt 107

```

```

<210> 51
<211> 204
<212> DNA
<213> Homo sapien

```

```

<400> 51
gtcctaggaa gtctagggga cacacgactc tggggtcacg gggccgacac acttgacagg 60

```


cggaaggaa aggcagagaa gtgacaccgt caggggggaaa tgacagaaag gaaaatcaag	120
gccttgcaag gtcagaaagg ggactcaggg cttccaccac agccctgccc cacttgcca	180
cctccctttt gggaccagca atgt	204

<210> 52
 <211> 491
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(491)
 <223> n = A,T,C or G

<400> 52	
acaaagataa catttatctt ataacaaaaa tttgatagtt ttaaagggtta gtattgtgta	60
gggtattttc caaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca	120
ccatcagaca gggtttttaa aaacaacata ttacaaaatt agacaatcat ccttaaaaaa	180
aaaacttctt gtatcaattt cttttgttca aaatgactga ctttaantatt tttaaatatt	240
tcanaaacac ttcctcaaaa attttcaana tggtagcttt canatgtgcc ctcagtccca	300
atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc	360
atgcaacagt gtcttttctt tnttttttct tttttttttt ttacaggcac agaaactcat	420
caattttatt tggataacaa agggctccca aatttatattg aaaaataaat ccaagttaat	480
atcactcttg t	491

<210> 53
 <211> 484
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(484)
 <223> n = A,T,C or G

<400> 53	
acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga	60
gtattaacag ttggtgaagt ttggtatatt tatgcagcat tttctttttg ctttgataac	120
actacagaac ccttaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct	180
caatcaaate tctacataac actatagtaa ttaaaacggt aaaaaaaagt gttgaaatct	240
gcactagtat anaccgctcc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc	300
agctttgant tttttgtgc tgatangagg aaaggctgaa ttaccttggt goctctocct	360
aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccncc	420
tancttgant ctgtgtattc caggancagg cggatggaat gggccagccc ncggatgttc	480
cant	484

<210> 54
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 54	
actaaacctc gtgcttgtga actccatata gaaaacgggt ccateccctga acacggctgg	60
ccactgggta tactgctgac aaccgcaaca acaaaaacac aaatccttgg cactggctag	120
tctatgtcct ctcaagtgcc tttttgtttg t	151

<210> 55
 <211> 91
 <212> DNA
 <213> Homo sapien

<400> 55
 acctggcttg tctccgggtg gttccccggcg cccccccacgg tccccagaac ggacactttc 60
 gccctccagt ggatactcga gccaaagtgg t 91

<210> 56
 <211> 133
 <212> DNA
 <213> Homo sapien

<400> 56
 ggcggatgtg cggttggttat atacaaatat gtcattttat gtaagggact tgagtataact 60
 tggatttttg gtatctgtgg gttgggggga cggtcaggga accaataccc catggatacc 120
 aagggacaac tgt 133

<210> 57
 <211> 147
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(147)
 <223> n = A,T,C or G

<400> 57
 actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60
 gactgggagc tgagcccttc cctttgcgcc tgccctcagag gattgttgcc gacntgcana 120
 tctcantggg ctggatncat gcagggt 147

<210> 58
 <211> 198
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(198)
 <223> n = A,T,C or G

<400> 58
 acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60
 tgattacata catttacct ttaaaaaaga tgtaaatctt aatttttatg ccatctatta 120
 attaccaat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt 180
 ttgacttcta agtttggt 198

<210> 59
 <211> 330
 <212> DNA
 <213> Homo sapien

<400> 59

acaacaaatg ggttgtgagg aagtcttatac agcaaaactg gtgatggcta ctgaaaagat	60
ccattgaaaa ttatcattaa tgattttaaa tgacaagtta tcaaaaactc actcaatttt	120
cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa	180
tacagtcaat aaatgacaaa gccagggcct acaggtgggt tccagacttt ccagacccag	240
cagaaggaat ctattttatc acatggatct ccgtctgtgc tcaaaatacc taatgatatt	300
tttcgtcttt attggacttc tttgaagagt	330

<210> 60

<211> 175

<212> DNA

<213> Homo sapien

<400> 60

accgtgggtg ccttctacat tcttgacggc tccttcacca acatctgggt ctacttcggc	60
gtcgtgggt ccttctctt catctctatc cagctgggtg tgctcatcga ctttgcgcac	120
tcctggaacc agcgggtggc gggcaaggcc gaggagtgcg attcccgtgc ctggt	175

<210> 61

<211> 154

<212> DNA

<213> Homo sapien

<400> 61

accccacttt tcttctgtg agcagtcctg acttctcact gctacatgat gagggtagt	60
ggttggtgct cttcaacagt atcttccct ttcggatct gctgagcgg acagcagtcg	120
tggactgcac agccccgggg ctccacattg ctgt	154

<210> 62

<211> 30

<212> DNA

<213> Homo sapien

<400> 62

cgctcgagcc ctatagttag tctgtattaga	30
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<210> 63

<211> 89

<212> DNA

<213> Homo sapien

<400> 63

acaagtcatt tcagcacct ttgctcttca aaactgaoca tcttttatat ttaatgcttc	60
ctgtatgaat aaaaatgggt atgtcaagt	89

<210> 64

<211> 97

<212> DNA

<213> Homo sapien

<400> 64

accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa gggtctgcag	60
aatcagtgca tccaggattg gtcttggat ctgggggt	97

<210> 65
 <211> 377
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(377)
 <223> n = A,T,C or G

<400> 65
 acaacaanaa ntcccttctt taggccactg atggaaacct ggaacccccct tttgatggca 60
 gcatggcgctc ctaggccttg acacagcggc tgggggtttgg gctntcccaa accgcacacc 120
 ccaaccctgg tctaccaca nttctggcta tgggctgtct ctgccactga acatcagggc 180
 tcggtcataa natgaaatcc caanggggac agaggctcagt agaggaagct caatgagaaa 240
 ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg 300
 tgggggtgaa ctaccccccag gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360
 gggcgggagg agcatgt 377

<210> 66
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 66
 acgcctttcc ctccagaattc aggggaagaga ctgtcgctg ccttctctcg ttgttgcggtg 60
 agaacccgtg tgcccttcc caccatatcc accctcgctc catctttgaa ctcaaacacg 120
 aggaactaac tgcaccctgg tctctctccc agtccccagt tcaccctcca tccctcacct 180
 tcttccactc taagggatat caacactgcc cagcacaggg gccctgaatt tatgtgggtt 240
 ttatatattt ttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300
 tggtt 305

<210> 67
 <211> 385
 <212> DNA
 <213> Homo sapien

<400> 67
 actacacaca ctccacttgc ccttgtgaga cactttgtcc cagcacttta ggaatgctga 60
 ggtcggacca gccacatctc atgtgcaaga ttgcccagca gacatcaggt ctgagagttc 120
 cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180
 tgtgctgtgc tggagattca cttttgagag agttctctc tgagacctga tctttagagg 240
 ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300
 cctctcccag ggcccagcc tggccacacc tgcttacagg gcactctcag atgccatac 360
 catagtttct gtgctagtgg accgt 385

<210> 68
 <211> 73
 <212> DNA
 <213> Homo sapien

<400> 68
 acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60
 gtttttttaa tgg 73

<210> 69
 <211> 536
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(536)
 <223> n = A,T,C or G

<400> 69
 actagtccag tgtggtggaa ttccattgtg ttgggggctc tcaacctcct ctctgcagc 60
 tccagctttg tgctctgcct ctgaggagac catggcccag catctgagta ccctgctgct 120
 cctgctggcc accctagctg tggccctggc ctggagcccc aaggaggagg ataggataat 180
 cccgggtggc atctataacg cagacctcaa tgatgagtgg gtacagcgtg cccttcactt 240
 cgccatcagc gagtataaca aggccaccaa agatgactac tacagacgtc cgctgcgggg 300
 actaagagcc aggcacacaga ccgttggggg ggtgaattac ttcttcgacg tagaggtggg 360
 ccgaaccata tgtaccaagt cccagcccaa cttggacacc tgtgccttcc atgaacagcc 420
 agaactgcag aagaaacagt tgtgctcttt cgagatctac gaagtccct ggggagaaca 480
 gaangtcctt ggggtgaaac caggtgtcaa gaaatcctan ggatctgttg ccaggc 536

<210> 70
 <211> 477
 <212> DNA
 <213> Homo sapien
 <400> 70

atgaccccta acaggggccc tctcagccct cctaattgacc tccggcctag ccattgtgatt 60
 tcacttccac tccataacgc tctctatact aggcctacta accaacacac taaccatata 120
 ccaatgatgg cgcgatgtaa caccagaaaag cacataccaa ggccaccaca caccacctgt 180
 ccaaaaaggc cttcgatacg ggataatcct atttattacc tcagaagttt ttttcttcgc 240
 agggattttt ctgagccttt taccactcca gcctagcccc taccocccaa ctaggagggc 300
 actggcccc aacaggcatc accocgctaa atccocctaga agtcocactc ctaaaacacat 360
 ccgtattact cgcattcagga gtatcaatca cctgagctca ccattagtcta atagaaaaca 420
 accgaaacca aattattcaa agcactgctt attacaattt tactgggtct ctatttt 477

<210> 71
 <211> 533
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(533)
 <223> n = A,T,C or G

<400> 71
 agagctatag gtacagtgtg atctcagctt tgcaaacaca ttttctacat agatagtact 60
 aggtattaat agatattgtaa agaaagaaat cacaccatta ataattggtaa gattgggtta 120
 tgtgatttta gtggtatttt tggcacccct atatatgttt tccaaacttt cagcagtgat 180
 attatttoca taacttaaaaa agtgagtttg aaaaagaaaa tctccagcaa gcatctcatt 240
 taaataaagg tttgtcatct ttaaaaatac agcaatatgt gactttttta aaaagctgtc 300
 aaataggtgt gacctacta ataattatta gaaatacatt taaaaacatc gagtacctca 360
 agtcagtttg ccttgaaaaa tatcaaatat aactcttaga gaaatgtaca taaaagaatg 420
 cttcgtaatt ttggagtang aggttccttc ctcaattttg tattttttaa aagtacatgg 480
 taaaaaaaaa aattcacacac agtatataag gctgtaaaat gaagaattct gcc 533

<210> 72
 <211> 511
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(511)
 <223> n = A,T,C or G

<400> 72
 tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcgtgta 60
 aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa 120
 aagccgcagg atgtctacac tatancaggc gctatttggt ttggctggag gagctgtgga 180
 aaacatggan agattggtgc tgganacgc cgtggctatt cctcattgtt attacanagt 240
 gaggttctct gtgtgcccac tggtttgaaa accgttctnc aataatgata gaatagtaca 300
 cacatgagaa ctgaaatggc ccaaaccag aaagaaagcc caactagatc ctcagaanac 360
 gcttctaggg acaataaccg atgaagaaaa gatggcctcc ttgtgcccc gtctgttatg 420
 atttctctcc attgcagcna naaaccggtt cttctaagca aacncagggtg atgatggcna 480
 aaatacaccc cctcttgaag naccnggagg a 511

<210> 73
 <211> 499
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(499)
 <223> n = A,T,C or G

<400> 73
 cagtgccagc actggtgccg gtaccagtag caataacagt gccagtgccg gtgccagcac 60
 cagtgggtggc ttcagtgtcg gtgccagcct gaccgccact ctcacatttg ggctcttctgc 120
 tggccttggg ggagctgggt ccagcaccag tggcagctct ggtgcctgtg gtttctctta 180
 caagtgagat tttagatatt gttaatcctg ccagtccttc tctcaagcc aggggtgcac 240
 ctcagaaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagttgaca 300
 ctctgcatta aatctatttg ccatttctga aaaaaaaaaa aaaaaaaggg cggccgctcg 360
 antctagagg gcccggttaa acccgctgat cagcctcgac tgtgccttct anttgccagc 420
 catctgttgt ttgcccctcc cccgntgcct tccttgaccc tggaaagtgc cactcccact 480
 gtccttttct aantaaat 499

<210> 74
 <211> 537
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(537)
 <223> n = A,T,C or G

<400> 74
 tttcatagga gaacacactg aggagatact tgaagaatgt ggattcagcc gcgaagagat 60

ttatcagctt	aactcagata	aaatcattga	aagtaataag	gtaaaagcta	gtctctaact	120
tccaggccca	cggctcaagt	gaatttgaat	actgcattta	cagtgtagag	taacacataa	180
cattgtatgc	atggaaacat	ggaggaacag	tattacagt	tcctaccact	ctaatacaaga	240
aaagaattac	agactctgat	tctacagtga	tgattgaatt	ctaaaaatgg	taatcattag	300
ggcttttgat	ttataanact	ttgggtactt	atactaaatt	atggtagtta	tactgccttc	360
cagtttgctt	gatatatttg	ttgatattaa	gattcttgac	ttatattttg	aatgggttct	420
actgaaaaan	gaatgatata	ttcttgaaga	catcgatata	catttattta	cactcttgat	480
tctacaatgt	agaaaatgaa	ggaaatgccc	caaattgtat	ggtgataaaa	gtcccgct	537

<210> 75

<211> 467

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(467)

<223> n = A,T,C or G

<400> 75

caaanacaat	tgttcaaaaag	atgcaaatga	tacactactg	ctgcagctca	caaacacctc	60
tgcattattac	acgtacctcc	tctgtctcct	caagtagtgt	ggtctatttt	gccatcatca	120
cctgctgtct	gcttagaaga	acggctttct	gctgcaangg	agagaaatca	taacagacgg	180
tggcacaagg	aggccatctt	ttcctcatcg	gttattgtcc	ctagaagcgt	cttctgagga	240
tctagttggg	ctttctttct	gggtttgggc	catttcantt	ctcatgtgtg	tactattcta	300
tcattattgt	ataacgggtt	tcaaaccngt	gggcacncag	agaacctcac	tctgtaataa	360
caatgaggaa	tagccaagggt	gatctccage	accaaatctc	tccatgttnt	tccagagctc	420
ctccagccaa	cccaaatagc	cgctgctatn	gtgtagaaca	tccctgn		467

<210> 76

<211> 400

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(400)

<223> n = A,T,C or G

<400> 76

aagctgacag	cattcggggcc	gagatgtctc	gctocgtggc	cttagctgtg	ctcgcgctac	60
tctctctttc	tggcctggag	gctatccagc	gtactccaaa	gattcaggtt	tactcacgtc	120
atccagcaga	gaatggaaag	tcaaatttcc	tgaattgcta	tgtgtctggg	tttcatccat	180
ccgacattga	agttgactta	ctgaagaatg	gagagagaat	tgaaaaagtg	gagcattcag	240
acttgtcttt	cagcaaggac	tggtctttct	atctcttgta	ctacactgaa	ttcaccoccca	300
ctgaaaaaga	tgagtatgcc	tgccgtgtga	accatgtgac	tttgtcacag	cccaagatng	360
ttnagtggga	tcanacatg	taagcagcan	catgggaggt			400

<210> 77

<211> 248

<212> DNA

<213> Homo sapien

<400> 77

ctggagtgcc	ttggtgtttc	aagccctgac	aggaagcaga	atgcaocttc	tgaggcacct	60
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ccagctgccc cggcggggga tgcgaggctc ggagcaccct tgcccggctg tgattgctgc 120
caggcactgt tcattctcagc ttttctgtcc ctttgtcccc ggcaagcgct tctgctgaaa 180
gttcataatct ggagcctgat gtcttaacga ataaagggtcc catgctccac ccgaaaaaaa 240
aaaaaaaaa 248

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<210> 78
<211> 201
<212> DNA
<213> Homo sapien

```

```

<400> 78
actagtccag tgtgggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca 60
tcaccagac cccgccctgc ccgtgcccga cgctgctgct aacgacagta tgatgcttac 120
tctgctactc ggaaactatt tttatgtaat taatgtatgc tttcttggtt ataatgcct 180
gatttaaaaa aaaaaaaaaa a 201

```

```

<210> 79
<211> 552
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (552)
<223> n = A,T,C or G

```

```

<400> 79
tccttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg 60
tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt 120
cctctttctt ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag 180
tgtgatagta taagtatcta agtgcagatg aaagtgtggt atatatatcc attcaaaatt 240
atgcaagtta gtaattactc agggttaact aaattacttt aatatgctgt tgaacctact 300
ctgttccttg gctagaaaaa attataaaca ggactttggt agtttgggaa gccaaattga 360
taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaatttta 420
ttcccaggaa tatgggggtc atttatgaat antaccggg anagaagttt tgantnaaac 480
cngttttggt taatacggtta atatgtcctn aatnaacaag gcntgactta tttccaaaaa 540
aaaaaaaaaa aa 552

```

```

<210> 80
<211> 476
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (476)
<223> n = A,T,C or G

```

```

<400> 80
acaggggattt gagatgctaa ggccccagag atcgtttgat ccaacctctt tattttcaga 60
gggggaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct 120
cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt 180
gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcacta 240
agggttaaact ttcccaccca gaaaaggcaa cttagataaa atcttagagt actttcatac 300
tcttctaagt cctcttccag cctcactttg agtccctcctt ggggggtgat aggaantntc 360

```


tcttggtttt	ctcaataaaa	tctctatcca	tctcatgttt	aatttggtac	gcntaaaaat	420
gctgaaaaaa	ttaaaatgtt	ctggtttcnc	tttaaaaaaa	aaaaaaaaaa	aaaaaa	476

<210> 81
 <211> 232
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(232)
 <223> n = A,T,C or G

tttttttttg	tatgccttcn	ctgtggngtt	attgttgctg	ccaccttga	ggagcccagt	60
ttctttctgta	tctttctttt	ctgggggatc	ttcctggctc	tgccoctcca	ttccagcct	120
ctcatcccca	tcttgcaatt	ttgctagggt	tgagggcgt	ttcctggtag	cccctcagag	180
actcagtcag	cgggaataag	tcctaggggt	ggggggtgtg	gcaagccggc	ct	232

<210> 82
 <211> 383
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(383)
 <223> n = A,T,C or G

aggcgggagc	agaagctaaa	gccaaagccc	aagaagagt	gcagtgccag	cactggtgcc	60
agtaccagta	ccaataacat	gccagtgcca	gtgocagcac	cagtgggtggc	ttcagtgtctg	120
gtgccagcct	gaccgccact	ctcacatttg	ggctcttcgc	tgcccttggg	ggagctgggt	180
ccagcaccag	tggcagctct	ggtgcctgtg	gtttctccta	caagtgagat	tttagatatt	240
gttaatcctg	ccagtctttc	tcttcaagcc	aggggtgcac	ctcagaaacc	tactcaacac	300
agcactctng	gcagccacta	tcaatcaatt	gaagttgaca	ctctgcatta	aatctatttg	360
ccatttcaaa	aaaaaaaaaa	aaa				383

<210> 83
 <211> 494
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(494)
 <223> n = A,T,C or G

accgaattgg	gaccgctggc	ttataagcga	tcatgtcttc	cagtattacc	tcaacgagca	60
gggagatcga	gtctatacgc	tgaagaaatt	tgaccgatg	ggacaacaga	cctgctcagc	120
ccatctgtct	cggttctccc	cagatgacaa	atctctoga	caacgaatca	ccatcaagaa	180
acgcttcaag	gtgctcatga	ccagcaacc	gcgcctgtc	ctctgagggt	ccttaaaactg	240
atgtcttttc	tgccacctgt	tacccctcgg	agactcogta	accaaactct	tccgactgtg	300
agccctgatg	cctttttgcc	agccatactc	tttggentcc	agtctctcgt	ggcgattgat	360

```

tatgcttgtg tgaggcaatc atggtggcat cacccatnaa gggaacacat ttganttttt 420
tttcncatat tttaaattac naccagaata nttcagaata aatgaattga aaaactctta 480
aaaaaaaaaa aaaa 494

```

```

<210> 84
<211> 380
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(380)
<223> n = A,T,C or G

```

```

<400> 84
gctggtagcc tatggcgtgg ccacggangg gctcctgagg cacgggacag tgacttccca 60
agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag 120
gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttcttg 180
gcacaccctc ctggggccca ggcgggcacc tgcgtctccc agtatgcaa ctggtgtgtg 240
gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctggtcac ttgctcattg 300
ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc 360
agcgttnccg cctcatccgg 380

```

```

<210> 85
<211> 481
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(481)
<223> n = A,T,C or G

```

```

<400> 85
gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggctctcgc ttcataccgc 60
tnccatcgtc atactgtagg ttggccacca cctcctgcat cttggggcgg ctaatatcca 120
ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tggttctgtc ttcgctcgg 180
tgtgaaagga tctccagaag gagtgtcga tcttccccac acttttgatg actttattga 240
gtcgattctg catgtccagc aggaggttgt accagctctc tgacagtga gtcaccagcc 300
ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggt gnagtctcac 360
ccagattctg cattaccaga nagccgtggc aaaaganatt gacaactcgc ccaggngaa 420
aaagaacacc tcttggaagt gctngccgct cctcgtcent tggtggnngc gentncctt 480
t 481

```

```

<210> 86
<211> 472
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(472)
<223> n = A,T,C or G

```

```

<400> 86

```

```

aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt      60
acttgaaaaa gcaacttnaa gcctggacac tggatttaa attcacaata tgcaaacatt      120
taaacagtgt gtcaatctgc tcccttactt tgtcatcaoc agtctgggaa taagggtatg      180
ccctattcac acctgttaaa agggcgctaa gcatttttga ttcaacatct tttttttga      240
cacaagtccg aaaaaagcaa aagtaaacag ttnttaattt gttagocaat tcactttctt      300
catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg      360
atatntgagc ggaagantag cctttctact tcaccagaca caactccttt catattggga      420
tgtnnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg      472

```

<210> 87

<211> 413

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(413)

<223> n = A,T,C or G

<400> 87

```

agaaaccagt atctctnaaa acaacctctc atacctgtg gacctaatth ttgtgtgcgtg      60
tgtgtgtgcg cgcataattat atagacaggc acatcttttt tacttttgta aaagcttatg      120
cctcttttgt atctatatct gtgaaagtth taatgatctg ccataatgtc ttggggacct      180
ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttingt      240
tttattcgac atgaaggaaa ttccagatn acaacctna caaactctcc cttagactagg      300
ggggacaaaag aaaagcnaaa ctgaacatna gaaacaattn cctggtgaga aattncataa      360
acagaaattg ggtngtatat tgaaanann catcattnaa acgttttttt ttt      413

```

<210> 88

<211> 448

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(448)

<223> n = A,T,C or G

<400> 88

```

cgcagcgggt cctctctatc tagctccagc ctctcgcgtg coeactccc cgcgtccgcg      60
gtcctagccn accatggccg ggccctgctg cgcctcgctg ctctgctgg ccactcctggc      120
cgtggccctg gccgtgagcc ccgcggccgg ctccagctcc ggcaagcgc cgcgectggt      180
gggaggccca tggaccccg gtggaagaag aaggtgtgct gcgtgcactg gactttgccc      240
tcggcnanta caacaaaccc gcaacnactt ttaccnagcn cgcgtgcag gttgtgcgc      300
cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctgg gccaaacnng      360
tttaccagaa ccnagccaat tngaacaatt nccctccat aacagccct tttaaaaagg      420
gaancantcc tgntcttttc caaattht      448

```

<210> 89

<211> 463

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(463)

<223> n = A,T,C or G

<400> 89

gaattttgtg	cactggccac	tgtgatggaa	ccattgggcc	aggatgcttt	gagtttatca	60
gtagtgattc	tgccaaagtt	ggtgttgtaa	catgagtatg	taaaatgtca	aaaaattagc	120
agaggtctag	gtctgcatat	cagcagacag	tttgccgtg	tattttgtag	ccttgaagtt	180
ctcagtgaca	agttntttct	gatgcgaagt	tctnattcca	gtgttttagt	cctttgcatc	240
tttnatgtn	agacttgcct	ctntnaaatt	gcttttgtnt	tctgcaggta	ctatctgtgg	300
tttaacaaaa	tagaannact	tctctgcttn	gaanatttga	atatcttaca	tctnaaaatn	360
aattctctcc	ccatannaaa	acccangccc	ttggganaat	ttgaaaaang	gntccttcnn	420
aattcnnana	anttcagntn	tcatacaaca	naacngganc	ccc		463

<210> 90

<211> 400

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(400)

<223> n = A,T,C or G

<400> 90

agggattgaa	ggtctnttnt	actgtcggac	tgttcancca	ccaactctac	aagttgctgt	60
cttccactca	ctgtctgtaa	gcntnttaac	ccagactgta	tcttcataaa	tagaacaaat	120
tcttcaccag	tcacatcttc	taggaccttt	ttggattcag	ttagtataag	ctcttccact	180
tcctttgtta	agacttcate	tggtaaagtc	ttaagtittg	tagaaaggaa	tttaattgct	240
cgttctctaa	caatgtcctc	tccttgaaagt	atttggttga	acaacccacc	tnaagtcctt	300
ttgtgcatcc	attttaataa	tacttaatat	ggcattggtn	cactagggtta	aattctgcaa	360
gagtcactctg	tctgcaaaaag	ttgcgttagt	atatctgcca			400

<210> 91

<211> 480

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(480)

<223> n = A,T,C or G

<400> 91

gagctcggat	ccaataatct	ttgtctgagg	gcagcacaca	tatncagtgc	catggnaact	60
ggtctacccc	acatgggagc	agcatgccgt	agntatataa	ggtcattccc	tgagtcagac	120
atgcctcttt	gactaccgtg	tgccagtgtc	ggtgattctc	acacacctcc	nncgcctctt	180
tgtggaaaaa	ctggcacttg	nctggaaacta	gcaagacatc	acttacaaat	tcacccacga	240
gacacttgaa	aggtgtaaca	aagcgactct	tgcattgctt	tttgtccctc	cggcaccagt	300
tgtcaatact	aacccgctgg	tttgccctcca	tcacatttgt	gatctgtagc	tctggatata	360
tctcctgaca	gtactgaaga	acttcttctt	ttgtttcaaa	agcaactctt	ggtgcctgtt	420
ngatcagggt	cccatttccc	agtcogaatg	ttcacatggc	atatnttact	tcccacaaaa	480

<210> 92

<211> 477

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(477)

<223> n = A,T,C or G

<400> 92

atacagccca	natccacca	cgaagatgcg	cttgttgact	gagaacctga	tgcggctact	60
ggtcccgctg	tagceccagc	gactctecac	ctgctggaag	cggttgatgc	tgcactcctt	120
cccacgcagg	cagcagcggg	gccgggtcaat	gaactccact	cgtggccttg	gggtgacggg	180
taantgcagg	aagaggctga	ccacctcgcg	gtccaccagg	atgcccgact	gtgcgggacc	240
tgcagcgaaa	ctcctcgatg	gtcatgagcg	ggaagcgaat	gangccocagg	gccttgocca	300
gaaccttccg	cctgttctct	ggcgtaacct	gcagctgctg	ccgctnacac	tggcctcg	360
accagcggac	aaacggcggt	gaacagccgc	acctcacgga	tgcccantgt	gtcgcgctcc	420
aggaacggcn	ccagcgtgtc	caggtcaatg	tgggtgaanc	ctccgcgggt	aatggcg	477

<210> 93

<211> 377

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(377)

<223> n = A,T,C or G

<400> 93

gaacggctgg	accttgctc	gcattgtgct	gctggcagga	ataccttggc	aagcagctcc	60
agtcagagca	gccccagacc	gctgocgccc	gaagctaagc	ctgcctctgg	ccttccctc	120
cgcctcaatg	cagaaccant	agtgggagca	ctgtgtttag	agttaagagt	gaacactgtg	180
tgattttact	tgggaatttc	ctctgttata	tagcttttcc	caatgcta	ttccaaacaa	240
caacaacaaa	ataacatgtt	tgctgtttna	gttgataaaa	agtangtgat	tctgtatnta	300
aagaaaatat	tactgttaca	tatactgctt	gcaanttctg	tatttattgg	tnctctggaa	360
ataaatatat	tattaaa					377

<210> 94

<211> 495

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(495)

<223> n = A,T,C or G

<400> 94

ccctttgagg	ggttagggc	cagttcccag	tggaagaaac	aggccaggag	aantgcgtgc	60
cgagctgang	cagatttccc	acagtgaacc	cagagccctg	ggctatagtc	tctgaacctt	120
ccaaggaaag	accaccttct	ggggacatgg	gctggagggc	aggacctaga	ggcaccaagg	180
gaaggcocca	ttccggggct	gttcccgcag	gaggaagggg	aggggctctg	tgtgcccccc	240
acgaggaana	ggccctgant	cctgggatca	nacaccctt	cacgtgtatc	ccacacaaaa	300
tgcaagctca	ccaaggtccc	ctctcagtoc	cttccctaca	ccctgaacgg	ncactggocc	360
acaccacccc	agancancca	cccgcacatg	ggaatgttct	caaggaatcg	cngggcaacg	420
tggactctng	tccnnaagg	gggcagaatc	tccaatagan	gganngaacc	cttgctnana	480

aaaaaaaaana aaaaa

495

<210> 95
 <211> 472
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(472)
 <223> n = A,T,C or G

<400> 95
 gggtacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc 60
 cctctggaag ccttgccgag agcggacttt gtaattgttg gagaataact gctgaatttt 120
 tagctgtttt gagttgattc gcaccactgc accacaactc aatatgaaaa ctatttnact 180
 tatttattat cttgtgaaaa gtatacaatg aaaattttgt tcatactgta tttatcaagt 240
 atgatgaaaa gcaatagata tatattcttt tattatgttn aattatgatt gccattatta 300
 atcggcaaaa tgtggagtgt atgttctttt cacagtaata tatgcctttt gtaacttcac 360
 ttggttattt tattgtaaat gaattacaaa attcttaatt taagaaaatg gtangttata 420
 tttanttcan taatttcttt ccttgtttac gtaattttg aaaagaatgc at 472

<210> 96
 <211> 476
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(476)
 <223> n = A,T,C or G

<400> 96
 ctgaagcatt tcttcaaact tntctacttt tgtcattgat acctgtagta agttgacaat 60
 gtgggtgaaat ttcaaaatta tatgtaactt ctactagttt tactttctcc cccaagtctt 120
 ttttaactca tgattttttac acacacaatc cagaacttat tatatagcct ctaagtcttt 180
 attcttcaca gtagatgatg aaagagtcct ccagtgtctt gngcanaatg ttctagntat 240
 agctggatac atacngtggg agttctataa actcatacct cagtgggact naaccaaaat 300
 tgtgttagtc tcaattccta ccacactgag ggagcctccc aaatcactat attcttatct 360
 gcagggtact ctccagaaaa acngacaggg caggcttgca tgaaaaagtn acatctgcgt 420
 taaaaagtct atcttctcta nangtctgtn aaggaacaat ttaatcttct agcttt 476

<210> 97
 <211> 479
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(479)
 <223> n = A,T,C or G

<400> 97
 actcttttcta atgctgatat gatcttgagt ataagaatgc atatgtcact agaattggata 60
 aaataatgct gcaaaacttaa tgttcttatg caaaatggaa cgctaatagaa acacagctta 120

caatcgcaaa	tcaaaactca	caagtgtctca	tctgtttag	atttagtgta	ataagactta	180
gattgtgctc	cttcggatat	gattgtttct	canatcttgg	gcaatnttcc	ttagtcaaat	240
caggctacta	gaattctgtt	attggatatn	tgagagcatg	aaatttttaa	naatacactt	300
gtgattatna	aattaatcac	aaatttcact	tatacctgct	atcagcagct	agaaaaacat	360
ntnnttttta	natcaaagta	ttttgtgttt	ggaantgttn	aaatgaaatc	tgaatgtggg	420
ttcnatctta	ttttttccn	gacnactant	tnctttttta	gggnctattc	tganccatc	479

<210> 98

<211> 461

<212> DNA

<213> Homo sapien

<400> 98

agtgacttgt	cctccaacaa	aacccttga	tcaagtttgt	ggcactgaca	atcagacctt	60
tgctagttcc	tgtcatctat	tcgctactaa	atgcagactg	gaggggacca	aaaaggggca	120
tcaactccag	ctggattatt	ttggagcctg	caaactctatt	cctacttgta	cggactttga	180
agtgattcag	tttccctctac	ggatgagaga	ctggctcaag	aatacctca	tgacgcttta	240
tgaagccact	ctgaacacgc	tggttatcta	gatgagaaca	gagaaataaa	gtcagaaaat	300
ttacctggag	aaaagaggct	ttggctgggg	accatcccat	tgaaccttct	cttaaggact	360
ttaagaaaaa	ctaccacatg	ttgtgtatcc	tggtgccggc	cgtttatgaa	ctgaccaccc	420
tttgaataa	tcttgacgct	cctgaacttg	ctcctctgcy	a		461

<210> 99

<211> 171

<212> DNA

<213> Homo sapien

<400> 99

gtggccgcgc	gcaggtgttt	cctcgtaccg	cagggccccc	tccttcccc	aggcgctccct	60
cggcgctct	gcgggcccga	ggaggagcgg	ctggcgggtg	gggggagtg	gacccaccc	120
cggtgagaaa	agccttctct	agcgatctga	gaggcgtgcc	ttgggggtac	c	171

<210> 100

<211> 269

<212> DNA

<213> Homo sapien

<400> 100

cggccgcaag	tgcaactcca	gctggggccg	tgccgacgaa	gattctgcca	gcagttggtc	60
cgactgcgac	gacggcgggc	gcgacagtcg	caggtgcagc	gcgggcgcct	ggggtcttgc	120
aaggctgagc	tgacgccgca	gaggctcgtg	cacgtcocac	gaccttgacg	ccgtcgggga	180
cagccggaac	agagcccggg	gaagcgggag	gcctcgggga	gcacctcggg	aagggcggcc	240
cgagagatac	gcaggtgcag	gtggccgcc				269

<210> 101

<211> 405

<212> DNA

<213> Homo sapien

<400> 101

tttttttttt	ttttggaatc	tactgcgagc	acagcaggtc	agcaacaagt	ttattttgca	60
gctagcaagg	taacagggta	gggcatgggt	acatgttcag	gtcaacttcc	tttgtcgtgg	120
ttgattgggt	tgtctttatg	ggggcggggt	ggggtagggg	aaacgaagca	aataacatgg	180
agtgggtgca	coctccctgt	agaacctggg	tacaaagctt	ggggcagttc	acctgggtctg	240
tgaacctcat	tttcttgaca	tcaatgttat	tagaagtcag	gatattcttt	agagagtcca	300

ctgttctgga gggagattag gggttcttgc caaatccaac aaaatccact gaaaaagttg 360
 gatgatcagt acgaataccg aggcataatc tcatatcggg ggcca 405

<210> 102
 <211> 470
 <212> DNA
 <213> Homo sapien

<400> 102
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
 ggcacttaat ccattttttat ttcaaaatgt ctacaaattt aatcccatta tacggtattt 120
 tcaaaatcta aattattcaa attagccaaa tccttaccaa ataataccca aaaatcaaaa 180
 atatacttct ttcagcaaac ttgttacata aattaaaaaa atatatacgg ctggtgtttt 240
 caaagtacaa ttatcttaac actgcaaaaca ttttaaggaa ctaaaataaa aaaaaaact 300
 ccgcaaaggt taaagggaac aacaaattct tttacaacac cattataaaa atcatatctc 360
 aaatcttagg ggaatatata cttcacacgg gatcttaact tttactcact ttgtttattt 420
 ttttaacca ttgtttgggc ccaacacaat ggaatcccc ctggactagt 470

<210> 103
 <211> 581
 <212> DNA
 <213> Homo sapien

<400> 103
 tttttttttt ttttttttga cccccctctt ataaaaaaca agttaccatt ttatttttact 60
 tacacatatt tattttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac 120
 taaatggaaa ctgccttaga tacataattc ttaggaatta gcttaaaatc tgcctaaagt 180
 gaaaatcttc tctagctctt ttgactgtaa atttttgact cttgtaaaac atccaaattc 240
 atttttcttg tctttaaaat tatctaattc ttccattttt tccctattcc aagtcaattt 300
 gcttctctag cctcatttcc tagctcttat ctactattag taagtggctt ttttccctaaa 360
 agggaaaaca ggaagagaaa tggcacacaa aacaaacatt ttatattcat atttctacct 420
 acgttaataa aatagcattt tgtgaagcca gctcaaaaga aggcttagat ccttttatgt 480
 ccattttagt cactaaacga tatcaaagtg ccagaatgca aaaggtttgt gaacatttat 540
 tcaaaagcta atataagata tttcacatac tcatctttct g 581

<210> 104
 <211> 578
 <212> DNA
 <213> Homo sapien

<400> 104
 tttttttttt tttttttttt tttttctctt cttttttttt gaaatgagga tctagttttt 60
 cactctctag atagggcatg aagaaaactc atctttccag ctttaaaata acaatcaaat 120
 ctcttatgct atatcatatt ttaagttaaa ctaatgagtc actggcttat cttctctga 180
 aggaaatctg ttcattcttc tcattcatat agttatatca agtactacct tgcataattga 240
 gaggtttttc ttctctattt acacatatat ttccatgtga atttgtatca aacctttatt 300
 ttcatgcaaa ctagaaaata atgtttcttt tgcataagag aagagaacaa tatagcatta 360
 caaaactgct caaattgttt gttaagttat ccattataat tagttggcag gagctaatac 420
 aaatcacatt tacgacagca ataataaaac tgaagtacca gttaaatatc caaaaataatt 480
 aaaggaacat ttttagcctg ggtataatta gctaattcac tttacaagca tttattagaa 540
 tgaattcaca tggtattatt cctagcccaa cacaatgg 578

<210> 105
 <211> 538
 <212> DNA

<213> Homo sapien

<400> 105

tttttttttt	tttttcagta	ataatcagaa	caatatattat	ttttatattt	aaaattcata	60
gaaaagtgcc	ttacatttaa	taaaagtttg	tttctcaaag	tgatcagagg	aattagatat	120
gtcttgaaca	ccaatattaa	tttgaggaaa	atacaccaaa	atacattaag	taaattattt	180
aagatcatag	agcttgtaag	tgaaaagata	aaatttgacc	tcagaaactc	tgagcattaa	240
aaatccacta	ttagcaataa	aattactatg	gacttcttgc	tttaattttg	tgatgaatat	300
ggggtgtcac	tggtaaacca	acacattctg	aaggatacat	tacttagtga	tagattctta	360
tgtactttgc	taatacgtgg	atatgagttg	acaagtttct	ctttcttcaa	tcttttaagg	420
ggcgagaaat	gaggaagaaa	agaaaaggat	tacgcatact	gttctttcta	tggaaggatt	480
agatatgttt	cctttgccaa	tattaaaaaa	ataataatgt	ttactactag	tgaaaccc	538

<210> 106

<211> 473

<212> DNA

<213> Homo sapien

<400> 106

tttttttttt	ttttttagtc	aagtttctat	ttttattata	attaaagtct	tggtcatttc	60
atttattagc	tctgcaactt	acatatattaa	attaaagaaa	cgttttagac	aactgtacaa	120
tttataaatg	taagggtgcca	ttattgagta	atatattcct	ccaagagtgg	atgtgtccct	180
tctccacca	actaatgaac	agcaacatta	gtttaatttt	attagtagat	atacactgct	240
gcaaacgcta	attctcttct	ccatcccat	gtgatattgt	gtatatgtgt	gagttggtag	300
aatgcatcac	aatctacaat	caacagcaag	atgaagctag	gctgggcttt	cggtgaaaat	360
agactgtgtc	tgtctgaatc	aaatgatctg	acctatcctc	ggtggcaaga	actcttcgaa	420
ccgcttctc	aaaggcgctg	ccacatttgt	ggctctttgc	acttgtttca	aaa	473

<210> 107

<211> 1621

<212> DNA

<213> Homo sapien

<400> 107

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<210> 108
<211> 382
<212> PRT
<213> Homo sapien

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<400> 108
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Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20     25     30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35     40     45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50     55     60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65     70     75     80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85     90     95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100    105    110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115    120    125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130    135    140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145    150    155    160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165    170    175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180    185    190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195    200    205
Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
210    215    220
Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
225    230    235    240
Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
245    250    255
Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
260    265    270
Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
275    280    285
Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
290    295    300
His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
305    310    315    320
Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala

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325 330 335
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
 340 345 350
 Ile Leu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
 355 360 365
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
 370 375 380

<210> 109
 <211> 1524
 <212> DNA
 <213> Homo sapien

<400> 109
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<210> 110
 <211> 3410
 <212> DNA
 <213> Homo sapien

<400> 110
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<210> 111

<211> 1289

<212> DNA

<213> Homo sapien

<400> 111

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tgttacaatg	ttaaaaaaaa	aaaaaaaaaa				1289

<210> 112

<211> 315

<212> PRT

<213> Homo sapien

<400> 112

Met	Val	Phe	Thr	Val	Arg	Leu	Leu	His	Ile	Phe	Thr	Val	Asn	Lys	Gln
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Leu	Gly	Pro	Lys	Ile	Val	Ile	Val	Ser	Lys	Met	Met	Lys	Asp	Val	Phe
			20					25					30		
Phe	Phe	Leu	Phe	Phe	Leu	Gly	Val	Trp	Leu	Val	Ala	Tyr	Gly	Val	Ala
			35				40						45		
Thr	Glu	Gly	Leu	Leu	Arg	Pro	Arg	Asp	Ser	Asp	Phe	Pro	Ser	Ile	Leu
			50				55				60				
Arg	Arg	Val	Phe	Tyr	Arg	Pro	Tyr	Leu	Gln	Ile	Phe	Gly	Gln	Ile	Pro
65					70					75				80	
Gln	Glu	Asp	Met	Asp	Val	Ala	Leu	Met	Glu	His	Ser	Asn	Cys	Ser	Ser
				85						90				95	
Glu	Pro	Gly	Phe	Trp	Ala	His	Pro	Pro	Gly	Ala	Gln	Ala	Gly	Thr	Cys
			100					105					110		
Val	Ser	Gln	Tyr	Ala	Asn	Trp	Leu	Val	Val	Leu	Leu	Leu	Val	Ile	Phe
			115				120					125			
Leu	Leu	Val	Ala	Asn	Ile	Leu	Leu	Val	Asn	Leu	Leu	Ile	Ala	Met	Phe
			130				135					140			
Ser	Tyr	Thr	Phe	Gly	Lys	Val	Gln	Gly	Asn	Ser	Asp	Leu	Tyr	Trp	Lys
145					150					155				160	
Ala	Gln	Arg	Tyr	Arg	Leu	Ile	Arg	Glu	Phe	His	Ser	Arg	Pro	Ala	Leu
				165					170					175	
Ala	Pro	Pro	Phe	Ile	Val	Ile	Ser	His	Leu	Arg	Leu	Leu	Leu	Arg	Gln
			180					185					190		
Leu	Cys	Arg	Arg	Pro	Arg	Ser	Pro	Gln	Pro	Ser	Ser	Pro	Ala	Leu	Glu

195	200	205
His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr		
210	215	220
Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp		
225	230	235
Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val		
245	250	255
Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg		
260	265	270
Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly		
275	280	285
Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly		
290	295	300
Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp		
305	310	315

<210> 113
 <211> 553
 <212> PRT
 <213> Homo sapien

<400> 113

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala	
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20	25
Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val	
35	40
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly	
50	55
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly	
65	70
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile	
85	90
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu	
100	105
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly	
115	120
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu	
130	135
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala	
145	150
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr	
165	170
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu	
180	185
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu	
195	200
Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly	
210	215
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His	
225	230
Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu	
245	250
Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg	
	255

260 265 270
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
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 530 535 540
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 545 550

<210> 114

<211> 241

<212> PRT

<213> Homo sapien

<400> 114

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 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 35 40 45
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
 50 55 60
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
 65 70 75 80
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile

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      85      90      95
Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
      100      105      110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
      115      120      125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
      130      135      140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
      145      150      155      160
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
      165      170      175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
      180      185      190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
      195      200      205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
      210      215      220
Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
      225      230      235      240
Gln

```

<210> 115
 <211> 366
 <212> DNA
 <213> Homo sapien

```

<400> 115
gctctttctc tcccctcctc tgaatttaat tctttcaact tgcaatttgc aaggattaca      60
catttcactg tgatgtatat tgtgttgcaa aaaaaaaaaa gtgtctttgt ttaaaattac      120
ttggtttggt aatccatctt gcttttcccc cattggaact agtcattaac ccatctctga      180
actggtagaa aaacatctga agagctagtc tatcagcatc tgacagggtga attggatggt      240
tctcagaacc atttcaccca gacagcctgt ttctatcctg tttaataaat tagtttgggt      300
tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt      360
ttagtc                                         366

```

<210> 116
 <211> 282
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (282)
 <223> n = A,T,C or G

```

<400> 116
acaaagatga accatttcct atattatagc aaaattaataa tctacccgta ttctaattatt      60
gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa      120
agactttact attttcatat tttaagacac atgatttatc ctatttttagt aacctggttc      180
atacgttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt      240
tcaatctnga actatctana tcacagacat ttctatttct tt                                         282

```

<210> 117
 <211> 305

<212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(305)
 <223> n = A,T,C or G

<400> 117
 acacatgtcg cttcactgcc ttcttagatg cttctgggtca acatanagga acagggacca 60
 tatttatcct cctcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa 120
 aataaggcaa aatatatgaa acaacagggtc tcgagatatt ggaaatcagt caatgaagga 180
 tactgatccc tgatcactgt cctaattgcag gatgtgggaa acagatgagg tcacctctgt 240
 gactgcccc gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat 300
 tgggt 305

<210> 118
 <211> 71
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(71)
 <223> n = A,T,C or G

<400> 118
 accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa 60
 aantcctggg t 71

<210> 119
 <211> 212
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(212)
 <223> n = A,T,C or G

<400> 119
 actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaaaccaca 60
 gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac 120
 agtaagctgg ccttctaat aaaagaaaat tgaaaggttt ctcactaanc ggaattaant 180
 aatggantca aganactccc aggcctcagc gt 212

<210> 120
 <211> 90
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(90)
 <223> n = A,T,C or G

<400> 120
 actcgttgca natcaggggc cccccagagt caccgttgca ggagtccttc tggctctgcc 60
 ctccgccggc gcagaacatg ctgggggtggt 90

<210> 121
 <211> 218
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(218)
 <223> n = A,T,C or G

<400> 121
 tgtancgtga anacgacaga nagggttgct aaaaatggag aanccttgaa gtcattttga 60
 gaataagatt tgctaaaaga tttgggggcta aaacatgggt attggggagac atttctgaag 120
 atatncangt aaattangga atgaattcat ggttcttttg ggaattcctt tacgatngcc 180
 agcatanact tcatgtgggg atancagcta cccttgta 218

<210> 122
 <211> 171
 <212> DNA
 <213> Homo sapien

<400> 122
 taggggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg 60
 catttgtag ctcatggaac aggaagtcgg atgggtggggc atcttcagtg ctgcatgagt 120
 caccaccccg gcgggggtcat ctgtgccaca ggtccctggt gacagtgcgg t 171

<210> 123
 <211> 76
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(76)
 <223> n = A,T,C or G

<400> 123
 tgtagcgtga agacnacaga atgggtgtgtg ctgtgctatc caggaacaca tttattatca 60
 ttatcaanta ttgtgt 76

<210> 124
 <211> 131
 <212> DNA
 <213> Homo sapien

<400> 124
 acctttcccc aaggccaatg tcctgtgtgc taactggccg gctgcaggac agctgcaatt 60
 caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt attctcttgg 120
 ttaagatttg t 131

<210> 125
 <211> 432
 <212> DNA
 <213> Homo sapien

<400> 125
 acttttatcta ctggctatga aatagatggg ggaaaattgc gttaccaact ataccactgg 60
 cttgaaaaag aggtgatagc tcttcagagg acttggtgact tttgctcaga tgctgaagaa 120
 ctacagtctg catttggcag aaatgaagat gaatttggat taaatgagga tgctgaagat 180
 ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg 240
 ctcttgaagt atcagtcact tttgagaatg tttcttagtt actgcatact tcatggatcc 300
 catgggtgggg gtcttgcacg tgtaagaatg gaattgattt tgcttttgca agaattctcag 360
 caggaaacat cagaaccact attttctagc cctctgtcag agcaaacctc agtgcctctc 420
 ctctttgctt gt 432

<210> 126
 <211> 112
 <212> DNA
 <213> Homo sapien

<400> 126
 acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60
 agtaagaatg atatttcccc ccagggatca ccaaatattt ataaaaattt gt 112

<210> 127
 <211> 54
 <212> DNA
 <213> Homo sapien

<400> 127
 accacgaaac cataaacaag atggaagcat caatccactt gccaaagcaca gcag 54

<210> 128
 <211> 323
 <212> DNA
 <213> Homo sapien

<400> 128
 acctcattag taattgtttt gttgtttcat ttttttctaa tgtctccctt ctaccagctc 60
 acctgagata acagaatgaa aatggaagga cagocagatt tctcctttgc tctctgctca 120
 ttctctctga agtctaggtt acocattttg gggaccatt ataggcaata aacacagttc 180
 ccaaagcatt tggacagttt cttgttgtgt tttagaatgg ttttcccttt tcttagcctt 240
 ttcttgcaaa aggtcactc agtcccttgc ttgctcagtg gactgggctc cccaggggct 300
 aggtgcctt cttttccatg tcc 323

<210> 129
 <211> 192
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (192)
 <223> n = A,T,C or G

<400> 129

```

acatacatgt gtgtatatatt ttaaatatca cttttgtatc actctgactt tttagcatac      60
tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc      120
tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg      180
gataaacaaa gt                                     192

```

<210> 130

<211> 362

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(362)

<223> n = A,T,C or G

<400> 130

```

ccctttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca      60
tataatgacg caacaaaaag gtgctgttta gtcctatggg tcagtttatg cccctgacaa      120
gtttccattg tgttttgccg atcttctggc taatcgtggg atcctccatg ttattagtaa      180
ttctgtattc cattttgtta acgcctggga gatgtaacct gctangaggc taactttata      240
cttatttaaa agctcttatt ttgtggtcat taaaatggca atttatgtgc agcactttat      300
tgcagcagga agcacgtgtg ggttggttgt aaagctcttt gctaacttta aaaagtaatg      360
gg                                     362

```

<210> 131

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 131

```

ctttttgaaa gatcgtgtcc actcctgtgg acatcttggt ttaatggagt ttcccatgca      60
gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaaatgaga      120
gttctcccag gttcgccctg ctgctccaag tctcagcagc agcctctttt aggaggcatc      180
ttctgaacta gattaaggca gcttgtaa atctgatgtgat ttggtttatt atccaactaa      240
cttccatctg ttatcactgg agaaagccca gactccccc ancgnggtacg gattgtgggc      300
atanaaggat tgggtgaagc tggcgttgtg gt                                     332

```

<210> 132

<211> 322

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(322)

<223> n = A,T,C or G

<400> 132

```

acttttgcca ttttgtatat ataaacaatc ttgggacatt ctctgaaaa ctaggtgtcc      60

```

```

agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat      120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggaoccttg tatctcgggt      180
tttagcaagt taaaatgaan atgacaggaa aggcttattt atcaacaaag agaagagttg      240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct agggaagcct      300
gtaacaatct acaattggtc ca                                     322

```

```

<210> 133
<211> 278
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(278)
<223> n = A,T,C or G

```

```

<400> 133
acaagccttc acaagttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt      60
cttgtttttc tttccatctg gctcctgggt tgacaatttg tggaaacaac tctattgcta      120
ctatttaaaa aaaatcacia atctttccct ttaagctatg ttnaattcaa actattcctg      180
ctattcctgt tttgtcaaag aaattatatt ttcaaaaata tgtntatttg tttgatgggt      240
cccacgaaac actaataaaa accacagaga ccagcctg                               278

```

```

<210> 134
<211> 121
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(121)
<223> n = A,T,C or G

```

```

<400> 134
gtttanaaaaa ctgttttagc tccatagagg aaagaatggt aaactttgta ttttaaaaca      60
tgattctctg aggttaaact tggttttcaa atgttatttt tacttgtatt ttgcttttgg      120
t                                     121

```

```

<210> 135
<211> 350
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(350)
<223> n = A,T,C or G

```

```

<400> 135
acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atoctataacc      60
atancaagtg gtgactgggt aagcgtgega caaagggtcag ctggcacatt acttgtgtgc      120
aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggtaactoca      180
gggtgcccc caactcctgc agocgctcct ctgtgccagn ccctgnaagg aactttcgtc      240
ccacctcaat caagccctgg gccatgctac ctgcaatttg ctgaacaaac gtttgctgag      300
ttccaagga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt                    350

```

<210> 136
 <211> 399
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(399)
 <223> n = A,T,C or G

<400> 136
 tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60
 gctgtgattg tatccgaata ntctcgtga gaaaagataa tgagatgacg tgagcagcct 120
 gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga 180
 cctggcggcc agccagccag ccacagggtgg gcttcttcct ttgtggtga caacnccaag 240
 aaaactgcag aggccccagg tcagggtgtna gtgggtangt gaccataaaa caccagggtgc 300
 tcccaggaac ccgggcaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg 360
 ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

<210> 137
 <211> 165
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(165)
 <223> n = A,T,C or G

<400> 137
 actggtgtgg tngggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt 60
 ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120
 ttggctggtc ccaactggtgg tcactgtcat tgggtggggt cctgt 165

<210> 138
 <211> 338
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(338)
 <223> n = A,T,C or G

<400> 138
 actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc 60
 ttaacttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccac 120
 tgctgggcag tctcccatgc cttccacagt gaaagggtc gagaaaaatc acatccaatg 180
 tcatgtgttt ccagccacac caaaagggtgc ttgggggtgga gggctggggg catananggt 240
 cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa 300
 aaaaactgat gccttttttt tttttttttg taaaattc 338

<210> 139
 <211> 382

<212> DNA

<213> Homo sapien

<400> 139

gggaatcttg	gtttttggca	tctggtttgc	ctatagccga	ggccactttg	acagaacaaa	60
gaaagggact	tcgagtaaga	aggtgattta	cagccagcct	agtgcccgaa	gtgaaggaga	120
attcaaacag	acctcgteat	tcctgggttg	agcctggteg	gtcaccgcc	tatcatctgc	180
atttgctta	ctcaggtgct	accggactct	ggccccgat	gtctgtagtt	tcacaggatg	240
ccttatttgt	cttctacacc	ccacagggcc	ccctacttct	tcggatgtgt	ttttaataat	300
gtcagctatg	tgccccatcc	tccttcacgc	cctccctccc	tttctacca	ctgctgagtg	360
gcctggaact	tgtttaaagt	gt				382

<210> 140

<211> 200

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (200)

<223> n = A,T,C or G

<400> 140

accaaancct	ctttctgttg	tgtnngattt	tactataggg	gttnngcttn	ttctaaanat	60
acttttcatt	taacancctt	tgtaagtgt	caggctgcac	tttgctccat	anaattattg	120
ttttcacatt	tcaacttgta	tgtgtttgtc	tcttanagca	ttggtgaaat	cacatatttt	180
atattcagca	taaaggagaa					200

<210> 141

<211> 335

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (335)

<223> n = A,T,C or G

<400> 141

actttatttt	caaaacactc	atatgttgca	aaaaacacat	agaaaaataa	agtttggtgg	60
gggtgctgac	taaacttcaa	gtcacagact	tttatgtgac	agattggagc	agggtttgtt	120
atgcatgtag	agaaccctaa	ctaatttatt	aaacaggata	gaaacaggct	gtctgggtga	180
aatggttctg	agaaccatcc	aattcacctg	tcagatgctg	atanactagc	tcttcagatg	240
tttttctacc	agttcagaga	tnngttaatg	actanttcca	atggggaaaa	agcaagatgg	300
attcacaac	caagtaattt	taaacaaaga	cactt			335

<210> 142

<211> 459

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (459)

<223> n = A,T,C or G

<400> 142
 accagggttaa tattgccaca tatatccttt ccaattgcgg gctaaacaga cgtgtattta 60
 gggttgttta aagacaaccc agcttaatat caagagaaat tgtgacctt catggagtat 120
 ctgatggaga aaacactgag ttttgacaaa tcttatttta ttcagatagc agtctgatca 180
 cacatgggtcc aacaacactc aaataataaa tcaaataatna tcagatgtta aagattgggtc 240
 ttcaaacatc atagccaatg atgccccgct tgcctataat ctctccgaca taaaaccaca 300
 tcaaacactc agtggccacc aaaccattca gcacagcttc cttactgtg agctgtttga 360
 agctaccagt ctgagcacta ttgactatnt ttttcangct ctgaatagct ctagggatct 420
 cagcanggggt gggaggaacc agctcaacct tggcgtant 459

<210> 143
 <211> 140
 <212> DNA
 <213> Homo sapien

<400> 143
 acatttcctt ccaccaagtc aggactcctg gcttctgtgg gagttcttat cacctgaggg 60
 aaatccaaac agtctctctt agaaaggaat agtgtcacca accccacca tctccctgag 120
 accatccgac ttcctgtgt 140

<210> 144
 <211> 164
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (164)
 <223> n = A,T,C or G

<400> 144
 acttcagtaa caacatacaa taacaacatt aagtgtatat tgccatcttt gtcattttct 60
 atctatacca ctctcccttc tgaaaacaan aatcactanc caatcactta taaaatttg 120
 aggcaattaa tccatatttg ttttcaataa ggaaaaaaag atgt 164

<210> 145
 <211> 303
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (303)
 <223> n = A,T,C or G

<400> 145
 acgtagacca tccaactttg tatttgtaat ggcaaacatc cagnagcaat tcttaaacia 60
 actggagggt atttatacc aattatccca ttcattaaca tgccctcctc ctgaggctat 120
 gcaggacagc tatcataagt cggcccaggc atccagatac taccatttgt ataaacttca 180
 gtaggggagt ccatccaagt gacagggtcta atcaaaggag gaaatggaac ataagcccag 240
 tagtaaaatn ttgcttagct gaaacagcca caaaagactt accgccgtgg tgattaccat 300
 caa 303

<210> 146

<211> 327
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(327)
 <223> n = A,T,C or G

<400> 146
 actgcagctc aattagaagt ggtctctgac ttctcatcanc ttctcoctgg gctccatgac 60
 actggcctgg agtgactcat tgctctgggt gggttgagaga gctcctttgc caacaggcct 120
 ccaagtcagg gctgggattt gtttcctttc cacattctag caacaatatg ctggccactt 180
 cctgaacagg gaggggtgga ggagccagca tggaacaagc tgccactttc taaagtagcc 240
 agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgacctgca ggatggaatg 300
 taggggtgag ctgtgtgact ctatggt 327

<210> 147
 <211> 173
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(173)
 <223> n = A,T,C or G

<400> 147
 acattgtttt tttagataa agcattgana gagctctcct taacgtgaca caatggaagg 60
 actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120
 atattcaagc acatatgtta tatattattc agttccatgt ttatagocata gtt 173

<210> 148
 <211> 477
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(477)
 <223> n = A,T,C or G

<400> 148
 acaaccactt tatctcatcg aatttttaac ccaaactcac tcaactgtgac ttctctatcct 60
 atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact 120
 gccctactac ctgctgcaat aatcacattc octtccctgtc ctgacctga agcattggg 180
 gtggtcctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgctcac 240
 nccanccac ctcaccgacc ccatcctctt acacagctac ctcccttgctc tctaaccoca 300
 tagattatnt ccaaattcag tcaattaagt tactattaac actctacccg acatgtocag 360
 caccactggg aagccttctc cagccaacac acacacacac acacacacac acacacatat 420
 ccaggcacag gctacctcat cttcacatc acccctttaa ttaccatgct atgggtgg 477

<210> 149
 <211> 207
 <212> DNA

<213> Homo sapien

<400> 149

```
acagttgtat tataatatca agaaataaac ttgcaatgag agcattttaag agggaagaac      60
taacgtatatt tagagagcca aggaaggttt ctgtggggag tgggatgtaa ggtggggcct      120
gatgataaat aagagtcagc caggtaagtg ggtggtgtgg tatgggcaca gtgaagaaca      180
tttcaggcag agggaacagc agtgaaa                                           207
```

<210> 150

<211> 111

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (111)

<223> n = A,T,C or G

<400> 150

```
accttgattt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg      60
cacttaaatg tggtcagtgt ttggacttgt taactantgg catctttggg t                111
```

<210> 151

<211> 196

<212> DNA

<213> Homo sapien

<400> 151

```
agcgcggcag gtcattattga acattccaga tacctatcat tactcgatgc tgttgataac      60
agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat      120
ggataccaac cggaaaaccc ctatcccga cagcccactg tggccccac tgtctacgag      180
gtgcatccgg ctcagt                                                         196
```

<210> 152

<211> 132

<212> DNA

<213> Homo sapien

<400> 152

```
acagcacttt cacatgtaag aaggagagaaa ttcctaaatg taggagaaag ataacagAAC      60
cttccccctt tcatctagtg gtggaaacct gatgctttat gttgacagga atagaaccag      120
gaggagagtt gt                                                         132
```

<210> 153

<211> 285

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (285)

<223> n = A,T,C or G

<400> 153

```
acaanacca nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag      60
```

cttctgctct	tatgtcctca	tctgacaact	ctttaccatt	tttatcctcg	ctcagcagga	120
gcacatcaat	aaagtccaaa	gtcttggact	tggecttggc	ttggaggaag	tcataaacac	180
cctggctagt	gaggggtcgg	cgccgctcct	ggatgacggc	atctgtgaag	tcgtgcacca	240
gtctgcaggc	cctgtggaag	cgccgtccac	acggagtnag	gaatt		285

<210> 154

<211> 333

<212> DNA

<213> Homo sapien

<400> 154

accacagtcc	tggtgggcca	gggcttcatg	accccttctg	tgaaaagcca	tattatcacc	60
accccaaatt	tttccttaaa	tatctttaac	tgaagggggc	agcctcttga	ctgcaaagac	120
cctaagccgg	ttacacagct	aactccact	ggccctgatt	tgtgaaattg	ctgtgcctg	180
attggcacag	gagtcgaagg	tggtcagctc	ccctcctccg	tggaacgaga	ctctgatttg	240
agtttcacaa	attctcgggc	cacctcgta	ttgtcctct	gaaataaaat	ccggagaatg	300
gtcaggcctg	tctcatocat	atggatcttc	cgg			333

<210> 155

<211> 308

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(308)

<223> n = A,T,C or G

<400> 155

actggaaata	ataaaaccca	catcacagtg	ttgtgtcaaa	gatcatcagg	gcatggatgg	60
gaaagtgctt	tggaactgt	aaagtgccta	acacatgac	gatgattttt	gttataatat	120
ttgaatcacg	gtgcatacaa	actctcctgc	ctgtcctcc	tgggccocag	ccccagcccc	180
atcacagctc	actgctctgt	tcatccaggc	ccagcatgta	gtggctgatt	cttcttggct	240
gcttttagcc	tccanaagtt	tctctgaagc	caaccaaacc	tctangtgta	aggcatgctg	300
gccttggt						308

<210> 156

<211> 295

<212> DNA

<213> Homo sapien

<400> 156

accttgctcg	gtgcttggaa	catattagga	actcaaaata	tgagatgata	acagtgccta	60
ttattgatta	ctgagagaac	tgtagacat	ttagttgaag	atcttctaca	caggaactga	120
gaataggaga	ttatgtttgg	ccctcatatt	ctctcctatc	ctccttgctt	cattctatgt	180
ctaatatatt	ctcaatcaaa	taaggtagc	ataatcagga	aatcgaocaa	ataccaatat	240
aaaaccagat	gtctatcctt	aagattttca	aatagaaaac	aaattaacag	actat	295

<210> 157

<211> 126

<212> DNA

<213> Homo sapien

<400> 157

acaagtttaa	atagtgtgt	cactgtgcat	gtgctgaaat	gtgaaatcca	ccacatttct	60
------------	-----------	------------	------------	------------	------------	----

gaagagcaaa acaaattctg tcatgtaatc tctatcttgg gtcgtgggta tatctgtccc 120
cttagt 126

<210> 158
<211> 442
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(442)
<223> n = A,T,C or G

<400> 158
accactggt cttggaaaca cccatcctta atacgatgat ttttctgtcg tgtgaaaatg 60
aanccagcag gctgccccta gtcagtcctt ccttccagag aaaaagagat ttgagaaagt 120
gcctgggtaa ttcaccatta atttcctccc ccaaactctc tgagtcttcc cttaatatatt 180
ctggtggttc tgaccaaagc aggtcatggt ttgttgagca tttgggatcc cagtgaagta 240
natgtttgta gccttgcata cttagccctt cccacgcaca aacggagtgg cagagtgggtg 300
ccaaccctgt tttcccagtc cacgtagaca gattcacagt gcggaattct ggaagctgga 360
nacagacggg ctctttgcag agccgggact ctgagangga catgagggcc tctgcctctg 420
tgttcattct ctgatgtcct gt 442

<210> 159
<211> 498
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(498)
<223> n = A,T,C or G

<400> 159
acttccaggt aacgttggtg tttccgttga gcctgaactg atgggtgacg ttgtagggttc 60
tccaacaaga actgaggttg cagagcgggt aggggaagagt gctgttccag ttgcacctgg 120
gctgctgtgg actgttggtg attcctcact acggcccaag gttgtggaac tggcanaaag 180
gtgtgtgtgt gganttgagc tcgggcggct gtggtagggt gtgggctctt caacaggggc 240
tgctgtggtg ccggggangtg aangtggtgt gtcacttgag cttggccagc tctggaaagt 300
antanattct tcctgaaggc cagcgcttgt ggagctggca ngggtcantg ttgtgtgtaa 360
cgaaccagtg ctgctgtggg tgggtgtana tcctccacaa agcctgaagt tatggtgtcn 420
tcaggtaana atgtggtttc agtgtccctg ggcngctgtg gaaggttgta nattgtcacc 480
aagggaataa gctgtggt 498

<210> 160
<211> 380
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(380)
<223> n = A,T,C or G

<400> 160

```

acctgcatcc agcttccctg ccaaactcac aaggagacat caacctctag acagggaaac      60
agcttcagga tacttccagg agacagagcc accagcagca aaacaaatat tcccatgcct      120
ggagcatggc atagaggaag ctganaaatg tggggtctga ggaagccatt tgagtctggc      180
cactagacat ctcatcagcc acttgtgtga agagatgcc catgacccca gatgcctctc      240
ccacccttac ctccatctca cacacttgag ctttccactc tgtataattc taacatcctg      300
gagaaaaatg gcagtttgac cgaacctgtt cacaacggta gaggctgatt tctaacgaaa      360
cttgtagaat gaagcctgga

```

```

<210> 161
<211> 114
<212> DNA
<213> Homo sapien

```

```

<400> 161
actccacatc cectctgagc aggcggttgt cgttcaaggt gtatttgccc ttgcctgtca      60
cactgtccac tggccccctta tccacttggt gcttaatccc tcgaaagagc atgt      114

```

```

<210> 162
<211> 177
<212> DNA
<213> Homo sapien

```

```

<400> 162
actttctgaa tcgaatcaaa tgatacttag tgtagtttta atatcctcat atatatcaaa      60
gttttactac tctgataatt ttgtaaacca ggtaaccaga acatccagtc atacagcttt      120
tggtgatata taacttggca ataaccagc ctggtgatac ataaaactac tcactgt      177

```

```

<210> 163
<211> 137
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (137)
<223> n = A,T,C or G

```

```

<400> 163
cattataca gacaggcgtg aagacattca cgacaaaaac gcgaaattct atoccggtgac      60
canagaaggc agctacggct actoctacat cctggcggtg gtggccttcg cctgcacctt      120
catcagcggc atgatgt

```

```

<210> 164
<211> 469
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (469)
<223> n = A,T,C or G

```

```

<400> 164
cttatcacia tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgaactta      60
tgcaatgcat catgctatct catacctaat gagggagttc caggagattc aaocaggaaa      120

```

tgcattggatc	tcaaaggaaa	caaacaccca	ataaactcgg	agtggcagac	tgacaactgt	180
gagacatgca	cttgctacga	aacagaaatt	tcatgttgca	cccttgtttc	tacacctgtg	240
ggttatgaca	aagacaactg	ccaaagaatc	ttcaagaagg	aggactgcaa	gtatategtg	300
gtggagaaga	aggacccaaa	aaagacctgt	tctgtcagtg	aatggataat	ctaattgtgt	360
tctagtaggc	acagggctcc	caggccaggc	ctcattctcc	tctggcctct	aatagtcaat	420
gattgtgtag	ccatgcctat	cagtaaaaag	atntttgagc	aaacacttt		469

<210> 165

<211> 195

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (195)

<223> n = A,T,C or G

<400> 165

acagtttttt	atanatatcg	acattgcccg	cacttgtgtt	cagtttcata	aagctgggtg	60
atccgctgtc	atccactatt	ccttggttag	agtaaaaatt	attcttatag	cccattgtccc	120
tgcaggccgc	ccgcccgtag	ttctcgttcc	agtcgtcttg	gcacacaggg	tgccaggact	180
tcctctgaga	tgagt					195

<210> 166

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (383)

<223> n = A,T,C or G

<400> 166

acatcttagt	agtgtggcac	atcagggggc	catcagggtc	acagtcactc	atagcctcgc	60
cgaggctgga	gtccacacca	ccggtgtagg	tgtgtcfaat	cttgggcttg	gcgcccacct	120
ttggagaagg	gatatgctgc	acacacatgt	ccacaaagcc	tgtgaactcg	ccaaagaatt	180
tttgagacc	agcctgagca	aggggcggat	gttcagcttc	agtcctcct	tcgtcagggtg	240
gatgccaaac	tcgtctangg	tccgtgggaa	gctgggtgtc	acntcaccta	caacctgggc	300
gangatctta	taaagaggct	ccnagataaa	ctccacgaaa	cttctctggg	agctgctagt	360
nggggccttt	ttggtgaact	ttc				383

<210> 167

<211> 247

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (247)

<223> n = A,T,C or G

<400> 167

acagagccag	accttggcca	taaatgaanc	agagattaag	actaaacccc	aagtcganat	60
tggagcagaa	actggagcaa	gaagtgggccc	tggggctgaa	gtagagacca	aggccactgc	120

tatanccata	cacagagcca	actctcaggc	caaggcnatg	gttggggcag	anccagagac	180
tcaatctgan	tccaaagtgg	tggctggaac	actggtcatg	acanaggcag	tgactctgac	240
tgangtc						247

<210> 168
 <211> 273
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(273)
 <223> n = A,T,C or G

<400> 168						
acttctaagt	tttctagaag	tggaaggatt	gtantcatcc	tgaaaatggg	tttacttcaa	60
aatccctcan	ccttggttctt	cacnactgtc	tatactgana	gtgtcatgtt	tccacaaagg	120
gctgacacct	gagcctgnat	tttcaactcat	ccctgagaag	ccctttccag	taggggtggc	180
aattcccaac	ttccttgcca	caagcttccc	aggctttctc	ccctggaaaa	ctccagcttg	240
agtcaccgat	acactcatgg	gctgccttgg	gca			273

<210> 169
 <211> 431
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(431)
 <223> n = A,T,C or G

<400> 169						
acagccttgg	cttccccaaa	ctccacagtc	tcagtgcaga	aagatcatct	tccagcagtc	60
agctcagacc	aggggtcaaag	gatgtgacat	caacagtttc	tggtttcaga	acagggttcta	120
ctactgtcaa	atgaccoccc	atacttcctc	aaaggctgtg	gtaagttttg	cacagggtgag	180
ggcagcagaa	aggggggtant	tactgatgga	caccatcttc	tctgtatact	ccacactgac	240
cttgccatgg	gcaaaggccc	ctaccacaaa	aacaatagga	tcactgctgg	gcaccagctc	300
acgcacatca	ctgacaaccg	ggatggaaaa	agaantgccca	actttcatac	atocaaactgg	360
aaagtgatct	gatactggat	tcttaattac	cttcaaaaagc	ttctggggggc	catcagctgc	420
tcgaacactg	a					431

<210> 170
 <211> 266
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(266)
 <223> n = A,T,C or G

<400> 170						
acctgtgggc	tgggctgtta	tgcctgtgcc	ggctgctgaa	agggagttca	gagggtggagc	60
tcaaggagct	ctgcaggcat	tttgccaanc	ctctccanag	canaggggagc	aacctacact	120
ccccgctaga	aagacaccag	attggagtc	tgggaggggg	agttgggggtg	ggcattttgat	180

gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct 240
tcaaagctag gggctcggca ggtgga 266

<210> 171
<211> 1248
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(1248)
<223> n = A,T,C or G

<400> 171
ggcagccaaa tcataaacgg cgaggactgc agcccgccact cgcagccctg gcaggcggca 60
ctgggtcatgg aaaacgaatt gttctgctcg ggcgtcctgg tgcattccgca gtgggtgctg 120
tcagccgcac actgtttcca gaagtgaagt cagagctcct acaccatcgg gctgggcctg 180
cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta 240
cggcaccag agtacaacag acccttgctc gctaaccgacc tcatgctcat caagttggac 300
gaatccgtgt ccgagctga caccatccgg agcatcagca ttgcttcgca gtgccctacc 360
gcggggaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc 420
gtgctgcagt gcgtgaacgt gtcggtggtg tctgaggagg tctgcagtaa gctctatgac 480
ccgctgtacc accccagcat gttctgcgcc ggcggagggc aagaccagaa ggactcctgc 540
aacggtgact ctggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtcttcc 600
ggaaaagccc cgtgtggcca agttggcgtg ccagggtgtct acaccaacct ctgcaaattc 660
actgagtga tagagaaaac cgtccaggcc agttaactct ggggactggg aacccatgaa 720
attgaccccc aaatacatcc tgcggaagga attcaggaat atctgttccc agccctcct 780
ccctcaggcc caggagtcca ggccccagc cctcctccc tcaaaccaag ggtacagatc 840
cccagcccc cctccctcag acccaggagt ccagaccccc cagccccctc tccctcagac 900
ccaggagtcc agccctcct cctcagacc caggagtcca gacccccag cccctcctcc 960
ctcagaccca ggggtccagg cccccaaccc ctcctccctc agactcagag gtccaagccc 1020
ccaaccntc attccccaga ccagaggtc cagggtcccag cccctcntcc ctcagaccca 1080
gcggtccaat gccacctaga cntcctctgt acacagtgcc ccttctgtggc acgttgaccc 1140
aaccttacca gttggttttt catttttngt ccttttcccc tagatccaga aataaagttt 1200
aagagaagng caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1248

<210> 172
<211> 159
<212> PRT
<213> Homo sapien

<220>
<221> VARIANT
<222> (1)...(159)
<223> Xaa = Any Amino Acid

<400> 172
Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
1 5 10 15
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
20 25 30
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
35 40 45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
50 55 60

Arg	Met	Pro	Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu
65					70				75						80
Glu	Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe
			85					90						95	
Cys	Ala	Gly	Gly	Gln	Xaa	Gln	Xaa	Asp	Ser	Cys	Asn	Gly	Asp	Ser	
			100				105					110			
Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe
		115				120					125				
Gly	Lys	Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn
	130					135				140					
Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser	
145					150					155					

<210> 173
 <211> 1265
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1265)
 <223> n = A,T,C or G

<400> 173

ggcagcccg	actcgcagcc	ctggcaggcg	gcactgggtca	tggaaaacga	attgtttctgc	60
tggggcgctcc	tgggtgcatcc	gcagtgggtg	ctgtcagccg	cacactgttt	ccagaactcc	120
tacaccatcg	ggctgggcct	gcacagtctt	gaggccgacc	aagagccagg	gagccagatg	180
gtggaggcca	gcctctccgt	acggcaccca	gagtacaaca	gaccttctgt	cgctaacgac	240
ctcatgtctca	tcaagtggga	cgaatccgtg	tccgagtctg	acaccatccg	gagcatcagc	300
attgtttctgc	agtgccttac	cgcggggaac	tcttgcctcg	tttctggctg	gggtctgctg	360
gcgaacggtg	agctcacggg	tgtgtgtctg	ccctcttcaa	ggaggctctc	tgccagtcg	420
cgggggctga	cccagagctc	tgcgtcccag	gcagaatgcc	taccgtgctg	cagtgcgtga	480
acgtgtcggt	ggtgtctgag	gaggtctgca	gtaagctcta	tgacccgctg	taccacccca	540
gcatgtttctg	cgcggcgga	gggcaagacc	agaaggactc	ctgcaacggt	gactctgggg	600
ggccccgat	ctgcaacggg	tacttgacag	gocctgtgtc	tttcggaaaa	gccccgtgtg	660
gccaagttgg	cgtgccaggt	gtctacacca	acctctgcaa	attcactgag	tggatagaga	720
aaaccgtcca	ggccagttaa	ctctggggac	tgggaaccca	tgaaattgac	ccccaaatac	780
atcctgcgga	aggaattcag	gaatatctgt	tcccagcccc	tcttccctca	ggcccaggag	840
tccaggcccc	cagccccctc	tccctcaaac	caagggtaca	gatccccagc	ccctcctccc	900
tcagaccag	gagtcagac	cccccagccc	ctctccctc	agaccagga	gtccagoccc	960
tcctccntca	gaccagagg	tecagacccc	ccagccctc	ctocctcaga	ccagggggtt	1020
gaggccccca	acccctcctc	cttcagagtc	agagggtocaa	gcccccaaac	cctcgttccc	1080
cagaccagga	ggttnnaggtc	ccagccctc	tccntcaga	cccagnggtc	caatgccacc	1140
tagattttcc	ctgnacacag	tgcctccttg	tggngnggtg	acccaacctt	accagttggt	1200
ttttcatttt	tngtcccttt	cccctagatc	cagaaataaa	gtttaagaga	ngngcaaaaa	1260
aaaaa						1265

<210> 174
 <211> 1459
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1459)

<223> n = A,T,C or G

<400> 174

ggtcagccgc	acactgtttc	cagaagtgcg	tgcagagctc	ctacaccatc	gggctggggc	60
tgcacagtct	tgaggccgac	caagagccag	ggagccagat	ggaggaggcc	agcctctccg	120
tacggcacc	agagtacaac	agacccttgc	tcgctaacga	cctcatgctc	atcaagttgg	180
acgaatccgt	gtccgagtct	gacaccatcc	ggagcatcag	cattgcttcg	cagtgcccta	240
ccgcggggaa	ctcttgctc	gtttctggct	ggggtctgct	ggcgaacggg	gagctcacgg	300
gtgtgtgtct	gccctcttca	aggaggtcct	ctgcccagtc	gcgggggctg	accagagact	360
ctgcgtccca	ggcagaatgc	ctaccgtgct	gcagtgcgtg	aacgtgtcgg	tggtgtctga	420
ngaggtctgc	antaagctct	atgaccgcgt	gtaccacccc	ancatgttct	gcgccggcgg	480
agggcaagac	cagaaggact	cctgcaacgt	gagagagggg	aaaggggagg	gcaggcgact	540
cagggaaggg	tggagaaggg	ggagacagag	acacacaggg	ccgcatggcg	agatgcagag	600
atggagagac	acacagggag	acagtgcaca	ctagagagag	aaactgagag	aaacagagaa	660
ataaacacag	gaataaagag	aagcaaagga	agagagaaac	agaaacagac	atggggaggc	720
agaaacacac	acacatagaa	atgcagttga	ccttccaaca	gcatggggcc	tgaggggcgg	780
gacctccacc	caatagaaaa	tcctcttata	acttttgact	ccccaaaaac	ctgactagaa	840
atagcctact	gttgacgggg	agccttacca	ataacataaa	tagtcgattt	atgcatacgt	900
tttatgcatt	catgatatac	ctttgttgga	attttttgat	atttctaagc	tacacagttc	960
gtctgtgaat	ttttttaaat	tgttgcaact	ctcctaaaat	ttttctgatg	tgtttattga	1020
aaaaatccaa	gtataagtgg	acttgtgcat	tcaaaccagg	gttgttcaag	ggccaactgt	1080
gtacccagag	ggaaacagtg	acacagattc	atagaggtga	aacacgaaga	gaaacaggaa	1140
aatcaagac	tctacaaaga	ggctgggcag	gggtggctcat	gcctgtaatc	ccagcacttt	1200
gggaggcgag	gcaggcagat	cacttgagggt	aaggagtcca	agaccagcct	ggccaaaatg	1260
gtgaaatcct	gtctgtacta	aaaatacaaa	agttagctgg	atatggtggc	aggcgctgt	1320
aatcccagct	acttgggagg	ctgaggcagg	agaattgctt	gaatatggga	ggcagagggt	1380
gaagtgagtt	gagatcacac	cactatactc	cagctggggc	aacagagtaa	gactctgtct	1440
caaaaaaaaa	aaaaaaaaaa					1459

<210> 175

<211> 1167

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (1167)

<223> n = A,T,C or G

<400> 175

gcgcagccct	ggcaggcggc	actggtcag	gaaaacgaat	tggtctgctc	gggcgtcctg	60
gtgcatccgc	agtgggtgct	gtcagccgca	cactgtttcc	agaactccta	caccatcggg	120
ctgggcctgc	acagtcttga	ggccgaccaa	gagccaggga	gccagatggg	ggaggccagc	180
ctctccgtac	ggcaccacaga	gtacaacaga	ctcttgctcg	ctaaccgacct	catgctcatc	240
aagttggacg	aatccgtgtc	cgagtctgac	accatccgga	gcatcagcat	tgcttcgcag	300
tgcctaccg	cggggaactc	ttgcctcgtn	tctggctggg	gtctgctggc	gaacggcaga	360
atgcctaccg	tgctgcaactg	cgtgaacgtg	togggtgggt	ctgaggangt	ctgcagtaag	420
ctctatgacc	cgctgtacca	ccccagcatg	ttctgcgcgg	gcggaggggca	agaccagaag	480
gactcctgca	acgggtgactc	tggggggccc	ctgatctgca	acgggtactt	gcagggcctt	540
tggtctttcg	gaaaagcccc	gtgtggccaa	cttggcgtgc	caggtgtcta	caccaacctc	600
tgcaaatcca	ctgagtggtat	agagaaaacc	gtccagncca	gttaactctg	gggactggga	660
acccatgaaa	ttgaccacca	aatacatcct	gcggaangaa	ttcaggaata	tctgttccca	720
gcccctcctc	cctcaggccc	aggagtccag	gccccagcc	cctcctccct	caaaccaagg	780
gtacagatcc	ccagcccctc	ctccctcaga	cccaggagtc	cagaccccc	agcccctcnt	840
centcagacc	caggagtcca	gcccctcctc	cntcagacgc	aggagtccag	acccccagc	900

```

ccntcctccg tcagaccag ggggtgcaggc cccaacccc tcntcctca gagtcagagg      960
tccaagcccc caacccctcg ttccccagac ccagaggtnc aggtcccagc cctctctccc      1020
tcagaccag cggtccaatg ccacctagan tntccctgta cacagtgcgc ccttggtggca      1080
ngttgaccca accttaccag ttgggttttc attttttgtc cctttcccct agatccagaa      1140
ataaagtnta agagaagcgc aaaaaaa      1167

```

<210> 176
 <211> 205
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(205)
 <223> Xaa = Any Amino Acid

```

<400> 176
Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1          5          10          15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
          20          25          30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
          35          40          45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
          50          55          60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
          65          70          75          80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
          85          90          95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
          100          105          110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
          115          120          125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
          130          135          140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
          145          150          155          160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
          165          170          175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
          180          185          190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
          195          200          205

```

<210> 177
 <211> 1119
 <212> DNA
 <213> Homo sapien

```

<400> 177
gcgcaactcgc agccctggca ggcggcactg gtcattggaaa acgaattggt ctgctcgggc      60
gtcctgggtgc atccgcagtg ggtgctgtca gccgcacact gtttccagaa ctccctacacc      120
atcgggctgg gcctgcacag tcttgaggcc gacaaagagc cagggagcca gatgggtggag      180
gccagcctct ccgtacggca cccagagtag aacagaccct tgctcgtctaa cgacctcatg      240
ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tcoggagcat cagcattgct      300

```

```

tcgcagtgcc ctaccgcggg gaactcttgc ctcgtttctg gctgggggtct gctgggcgaac 360
gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc 420
caaccctggc aggggtgtac catttcggca acttccagtg caaggacgtc ctgctgcac 480
ctcactgggt gctcactact gctcactgca tcacccggaa cactgtgatc aactagccag 540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt 600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc 660
cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc 720
tgacctacag aggtgaggga tcatatagct cttcaaggat gctgggtactc ccctcacaaa 780
ttcattttct ctggtgtagt gaaagggtgc ccctctggag cctcccaggg tgggtgtgca 840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg 900
ctcagtacac cagggcaggt ctgacatttc ttcatttagt gtatgctgtc cattcatgca 960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg 1020
gaggtgaggg agagggccca tggttcaatg ggatctgtgc agttgtaaca cattaggtgc 1080
ttaataaaca gaagctgtga tgttaaaaaa aaaaaaaaaa 1119

```

<210> 178
 <211> 164
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(164)
 <223> Xaa = Any Amino Acid

```

<400> 178
Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1          5          10          15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20          25          30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35          40          45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
 50          55          60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65          70          75          80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85          90          95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
100          105          110
Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
115          120          125
Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
130          135          140
Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
145          150          155          160
Pro Gly Thr Leu

```

<210> 179
 <211> 250
 <212> DNA
 <213> Homo sapien

<400> 179

ctggagtgcc	tgggtgtttc	aagccccctgc	aggaagcaga	atgcaaccttc	tgaggcacct	60
ccagctgccc	ccggccgggg	gatgcgaggc	tcggagcacc	cttgcccggc	tgtgattgct	120
gccaggcact	gttcactctca	gcttttctgt	ccctttgctc	ccggcaagcg	cttctgctga	180
aagttcatat	ctggagcctg	atgtcttaac	gaataaagg	cccatgctcc	acccgaaaaa	240
aaaaaaaaa						250

<210> 180
 <211> 202
 <212> DNA
 <213> Homo sapien

<400> 180						
actagtccag	tgtggtggaa	ttccattgtg	ttgggcccac	cacaatggct	acctttaaca	60
tcacccagac	ccgccccctg	cccgtgcccc	acgctgctgc	taacgacagt	atgatgctta	120
ctctgctact	cggaaactat	ttttatgtaa	ttaatgtatg	ctttcttggt	tataaatgcc	180
tgatttaaaa	aaaaaaaaaa	aa				202

<210> 181
 <211> 558
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (558)
 <223> n = A,T,C or G

<400> 181						
tccytttgkt	naggtttkkg	agacamocck	agacctwaan	ctgtgtcaca	gacttcynngg	60
aatgttttagg	cagtgttagt	aatttcytcg	taatgattct	gttattactt	tcctnattct	120
ttattcctct	ttctcttgaa	gattaatgaa	gttgaaaatt	gaggtggata	aatacaaaaa	180
ggtagtgtga	tagtataagt	atctaagtc	agatgaaagt	gtgttatata	tatocattca	240
aaattatgca	agttagtaat	tactcaggg	taactaaatt	actttaatat	gctgttgaac	300
ctactctgtt	ccttggctag	aaaaaattat	aaacaggact	ttgttagttt	gggaagccaa	360
attgataata	ttctatgttc	taaaagttgg	gctatacata	aattattaag	aaatatggaw	420
ttttattccc	aggaatatgg	kgttcatttt	atgaatatta	cscrggatag	awgtwtgagt	480
aaaaycagtt	ttggtwaata	ygtwaatatg	tcmtaaataa	acaakgcttt	gacttatttc	540
caaaaaaaaa	aaaaaaaaa					558

<210> 182
 <211> 479
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (479)
 <223> n = A,T,C or G

<400> 182						
acagggwttk	grggatgcta	agscocccrga	rwtygtttga	tccaaocctg	gcttwttttc	60
agaggggaaa	atggggccta	gaagttacag	mscatytagy	tggtgcgmtg	gcacccctgg	120
cstcacacag	astcccagag	agctgggact	acaggcacac	agtcactgaa	gcaggccctg	180
ttwgcaattc	acgttgccac	ctocaaacta	aacattcttc	atatgtgatg	tccttagtca	240
ctaagggttaa	actttccac	ccagaaaagg	caacttagat	aaaatcttag	agtactttca	300

tactmttcta agtcctcttc cagcctcact kkgagtccctm cytggggggtt gataggaant	360
ntctcttggc tttctcaata aartctctat ycatctcatg ttttaatttgg tacgcatara	420
awtgstgara aaattaaaaat gttctgggty mactttaaaa araaaaaaaa aaaaaaaaaa	479

<210> 183

<211> 384

<212> DNA

<213> Homo sapien

<400> 183

aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactgggtgcc	60
agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtgggtgg cttcagtgc	120
gggtgccagcc tgaccgccac tctcacatctt gggctcttcg ctggccttgg tggagctggt	180
gccagcacca gtggcagctc tgggtgcctgt gggttctcct acaagtgaga ttttagatat	240
tgtaaatcct gccagtcttt ctcttcaagc caggggtgcat cctcagaaac ctactcaaca	300
cagcactcta ggcagccact atcaatcaat tgaagttgac actctgcatt aratctatctt	360
gccattttcaa aaaaaaaaaa aaaa	384

<210> 184

<211> 496

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(496)

<223> n = A,T,C or G

<400> 184

accgaattgg gaccgctggc ttataagcga tcatgtyynt ccrgtatkac ctcaacgagc	60
aggagatcg agtctatacg ctgaagaaat ttgacccgat gggacaacag acctgctcag	120
cccatcctgc tcgggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga	180
aacgcttcaa ggtgctcatg acccagcaac cgcgcctctg cctctgaggg tccettaaac	240
tgatgtcttt tctgccacct gttaccctc ggagactccg taaccaaact cttcggactg	300
tgagccctga tgcccttttg ccagccatac tctttggcat ccagtctctc gtggcgattg	360
attatgcttg tgtgaggcaa tcatgggtggc atcaccata aagggaacac atttgacttt	420
tttttctcat attttaaat actacmagaw tattwmagaw waaatgawtt gaaaaactst	480
taaaaaaaaa aaaaaa	496

<210> 185

<211> 384

<212> DNA

<213> Homo sapien

<400> 185

gctggtagcc tatggcgkkg cccacggagg ggctcctgag gccacggrac agtgacttcc	60
caagtatcyt gcgcsgcgtc ttctaccgtc cctacctgca gatcttcggg cagattcccc	120
aggaggacat ggacgtggcc ctcatggagc acagcaactg ytcgtcggag cccggcttct	180
gggcacaccc tcctggggcc caggcgggca cctgcgtctc ccagtatgcc aactggcttg	240
tggtgctgct cctcgtcatc ttctgctcg tggccaacat cctgctggtc aacttgctca	300
ttgccatgtt cagttacaca ttccggcaaag tacagggcaa cagcgatctc tactgggaag	360
gcgcagcgtt accgcctcat ccgg	384

<210> 186

<211> 577

<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (577)
<223> n = A,T,C or G

<400> 186

gagttagctc	ctccacaacc	ttgatgaggt	cgtctgcagt	ggcctctcgc	ttcataccgc	60
tnccatcgtc	atactgtagg	tttgccacca	cytcctggca	tcttggggcg	gcntaatatt	120
ccaggaaact	ctcaatcaag	tcaccgtcga	tgaaacctgt	gggctgggtc	tgtcttccgc	180
tcggtgtgaa	aggatctccc	agaaggagtg	ctcgatcttc	cccacacttt	tgatgacttt	240
attgagtcga	ttctgcatgt	ccagcaggag	gttgtaccag	ctctctgaca	gtgagggtcac	300
cagccctatc	atgccgttga	mcgtgocgaa	garcaccgag	ccttggtgtgg	gggkkggaagt	360
ctcacocaga	ttctgcatta	ccagagagcc	gtggcaaaaag	acattgacaa	actcgcccag	420
gtggaaaaag	amcamctcct	ggargtgctn	gccgctcctc	gtcmgttggt	ggcagcgctw	480
tccttttgac	acacaaaaca	gttaaaggca	ttttcagccc	ccagaaantt	gtcatcatcc	540
aagatntcgc	acagcactna	tccagttggg	attaaat			577

<210> 187
<211> 534
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (534)
<223> n = A,T,C or G

<400> 187

aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgstg	agaatycatw	60
actkggaaaa	gmaacattaa	agcctggaca	ctggatttaa	aattcacaat	atgcaacact	120
ttaaacagtg	tgtcaatctg	ctcccyynac	tttgtcatca	ccagtctggg	aakaagggtta	180
tgccctattc	acacctgtta	aaagggcgct	aagcattttt	gattcaacat	cttttttttt	240
gacacaagtc	cgaaaaaagc	aaaagtaaac	agttatyaat	ttgttagcca	attcactttc	300
ttcatgggac	agagccatyt	gatttaaaaa	gcaaattgca	taataattgag	cttyggggagc	360
tgatatattga	gcggaagagt	agccttttcta	cttcaecaga	cacaactccc	tttcatattg	420
ggatgttnac	naaagtwatg	tctctwacag	atgggatgct	tttgtggcaa	ttctgttctg	480
aggatctccc	agttttattta	ccacttgcac	aagaaggcgt	tttcttctctc	aggc	534

<210> 188
<211> 761
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1) ... (761)
<223> n = A,T,C or G

<400> 188

agaaaocagt	atctctnaaa	acaaoctctc	ataccttctg	gaocctaattt	tgtgtgcgtg	60
tgtgtgtgcg	cgcataattat	atagacaggc	acatcttttt	tacttttgta	aaagcttatg	120
cctcttttgg	atctatatct	gtgaaagttt	taatgatctg	ccataatgtc	ttggggacct	180

ttgtcttctg	tgtaaattggt	actagagaaa	acacctatnt	tatgagtcaa	tctagttngt	240
tttattcgac	atgaaggaaa	tttccagatn	acaacactna	caaactctcc	ctkgackarg	300
ggggacaaaag	aaaagcaaaa	ctgamcataa	raaacaatwa	cctgggtgaga	arttgcataa	360
acagaaatwr	ggtagtatat	tgaarnacag	catcattaaa	rmgttwtktt	wttctccctt	420
gcaaaaaaca	tgtacngact	tcccgttgag	taatgccaag	ttgttttttt	tatnataaaa	480
cttgcccttc	attacatggt	tnaaagtggg	gtgggtgggg	aaaatattga	aatgatggaa	540
ctgactgata	aagctgtaca	aataagcagt	gtgcctaaca	agcaacacag	taatgttgac	600
atgcttaatt	cacaaatgct	aatttcatta	taaatgtttg	ctaaaataca	ctttgaacta	660
tttttctgtn	ttcccagagc	tgagatntta	gattttatgt	agtatnaagt	gaaaaantac	720
gaaaaataata	acattgaaga	aaaananaaa	aaanaaaaaa	a		761

<210> 189

<211> 482

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(482)

<223> n = A,T,C or G

<400> 189

tttttttttt	tttgccgatn	ctactatntt	attgcaggan	gtgggggtgt	atgcaccgca	60
caccgggggt	atnagaagca	agaaggaagg	agggagggca	cagcccttg	ctgagcaaca	120
aagccgcctg	ctgccttctc	tgtctgtctc	ctgggtgcagg	cacatgggga	gaccttcccc	180
aaggcagggg	ccaccagtcc	aggggtggga	atacaggggg	tgggagtgt	gcataagaag	240
tgataggcac	aggccacccg	gtacagaccc	ctcggctcct	gacaggtnga	tttcgaccag	300
gtcattgtgc	cctgcccagg	cacagcgtan	atctggaaaa	gacagaatgc	tttccctttc	360
aaatttggt	ngtcatngaa	ngggcanttt	tccaanttng	gctnggtcct	ggtaacnctg	420
gttcggccca	gtccncgctc	caaaaantat	tcaccnntct	ccnaattgct	tgcnggnccc	480
cc						482

<210> 190

<211> 471

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(471)

<223> n = A,T,C or G

<400> 190

tttttttttt	ttttaaaaca	gtttttcaca	acaaaattta	ttagaagaat	agtgggtttg	60
aaaactctcg	catccagtga	gaactaccat	acaccacatt	acagctngga	atgtntctca	120
aatgtctggt	caaatgatac	aatggaacca	ttcaatctta	cacatgcacg	aaagaacaag	180
cgtttttgac	atacaatgca	caaaaaaaaa	aggggggggg	gaccacatgg	attaaaattt	240
taagtactca	tcacatacat	taagacacag	ttctagtcca	gtcnaaaatc	agaactgcnt	300
tgaaaaattt	catgtatgca	atccaaccaa	agaacttnat	tggtgatcat	gantnctcta	360
ctacatcnac	cttgatcatt	gccaggaacn	aaaagttnaa	ancacncngt	acaaaaanaa	420
tctgtaattn	anttcaacct	ccgtacngaa	aaatntntnt	tatacactcc	c	471

<210> 191

<211> 402

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(402)

<223> n = A,T,C or G

<400> 191

gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct	60
gtcttccact cactgtctgt aagcttttta aaccagacwg tatcttcata aatagaacaa	120
attcttcacc agtcacatct tctaggacct ttttggattc agttagtata agctcttcca	180
cttcctttgt taagacttca tctggtaaag tcttaagttt tgtagaaagg aattyaattg	240
ctcgttctct aacaatgtcc tctccttgaa gtatttggct gaacaaccca cctaaagtcc	300
ctttgtgcat ccattttaaa tatacttaat agggcattgk tncactaggt taaattctgc	360
aagagtcata tgtctgcaaa agttgcgta gtatatctgc ca	402

<210> 192

<211> 601

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(601)

<223> n = A,T,C or G

<400> 192

gagctcggat ocaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact	60
ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac	120
atgcytyttt gaytaccgtg tgccaagtgc tgggtgattct yaacacacyt ccatccgyt	180
cttttgtgga aaaactggca cttktctgga actagcarga catcacttac aaattcaccc	240
acgagacact tgaaagggtg aacaaaagcga ytcttgcatg gctttttgtc cctocggcac	300
cagttgtcaa tactaaccgg ctggtttgcc tccatcacat ttgtgatctg tagctctgga	360
tacatctcct gacagtactg aagaacttct tcttttgttt caaaagcacc tcttggtgcc	420
tggtggatca gggtcccatt tcccagtcyg aatgttcaca tggcatattt wacttcccac	480
aaaacattgc gatttgaggc tcagcaacag caaatcctgt tccggcattg gctgcaagag	540
cctcgatgta gccggccagc gccaaaggcag gcgcctgtag ccccaocagc agcagaagca	600
g	601

<210> 193

<211> 608

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(608)

<223> n = A,T,C or G

<400> 193

atacagccca natccacca cgaagatgcy ctgttgact gagaacctga tgcggtcact	60
ggtcccgtg tagccocagc gactctccac ctgctggaag cggttgatgc tgcactcytt	120
cccaacgcag gcagmagogg gsocggtcaa tgaactccay tctggtcttg gggtkgaegg	180
tkaagtgcag gaagaggctg accaactcgc ggtccaocag gatgcccagc tgtgcgggac	240
ctgcagcgaa actcctcgat ggtcatgagc ggaagcgaa tgaggcccag ggccttgecc	300

agaaccttcc	gcctgttctc	tggcgtcacc	tgcagctgct	gccgctgaca	ctcggcctcg	360
gaccagcgga	caaacggcrt	tgaacagccg	cacctcacgg	atgccagtg	tgtcgcgctc	420
caggammgsc	accagcgtgt	ccaggtcaat	gtcgggtgaag	cctccgcgg	gtrattggcgt	480
ctgcagtgtt	tttgtcgatg	ttctccaggc	acaggctggc	cagctgcggt	tcatacgaaga	540
gtcgcgcctg	cgtgagcagc	atgaaggcgt	tgtcggctcg	cagttcttct	tcaggaaactc	600
cacgcaat						608

<210> 194
 <211> 392
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(392)
 <223> n = A,T,C or G

<400> 194						
gaacggctgg	accttgccctc	gcattgtgct	tgctggcagg	gaataccttg	gcaagcagyt	60
ccagtcgag	cagccccaga	ccgctgccgc	ccgaagctaa	gcctgcctct	ggccttcccc	120
tccgcctcaa	tgcagaacca	gtagtgggag	cactgtgttt	agagttaaga	gtgaacactg	180
tttgatttta	cttggaatt	tctctgttta	tatagctttt	cccaatgcta	atttccaaac	240
aacaacaaca	aaataacatg	tttgccctgtt	aagttgtata	aaagtaggtg	attctgtatt	300
taaagaaaat	attactgtta	catatactgc	ttgcaatttc	tgtattttatt	gktnctstgg	360
aaataaatat	agttattaaa	ggttgtcant	cc			392

<210> 195
 <211> 502
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(502)
 <223> n = A,T,C or G

<400> 195						
ccsttkgagg	ggtkaggkyc	cagttyccga	gtggaagaaa	caggccagga	gaagtgcgtg	60
ccgagctgag	gcagatgttc	ccacagtgac	ccccagagcc	stgggstata	gtytctgacc	120
cctcncaagg	aaagaccacs	ttctggggac	atgggctgga	gggcaggacc	tagaggcacc	180
aagggaaggc	cccattccgg	ggstgttccc	cgaggaggaa	gggaaggggc	tctgtgtgcc	240
ccccasgagg	aagaggccct	gagtcctggg	atcacagacc	ccttcacgtg	tatccccaca	300
caaatagcaag	ctcaccaagg	tccccctca	gtcccccttc	stacaccctg	amcggccact	360
gscscacacc	cacccagagc	acgccacccg	ccatggggar	tgtgctcaag	gartcgcnng	420
gcarcgtgga	catctngtcc	cagaaggggg	cagaatctcc	aatagangga	ctgarcmstt	480
gctnanaaaa	aaaaanaaaa	aa				502

<210> 196
 <211> 665
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(665)

<223> n = A,T,C or G

<400> 196

ggttacttgg	tttcattgcc	accacttagt	ggatgtcatt	tagaaccatt	ttgtctgctc	60
cctctggaag	ccttgcgag	agcggacttt	gtaattggtg	gagaataact	gctgaatttt	120
wagctgtttk	gagttgatts	gcaccactgc	accacaact	tcaatatgaa	aacyawttga	180
actwatttat	tatcttgtga	aaagtataac	aatgaaaatt	ttgttcatac	tgtattkac	240
aagtatgatg	aaaagcaawa	gatatatatt	cttttattat	gttaaattat	gattgccatt	300
attaatcggc	aaaatgtgga	gtgtatgttc	ttttcacagt	aatatatgcc	ttttgtaact	360
tcacttggtt	attttattgt	aaatgartta	caaaaattctt	aatttaagar	aatggtagt	420
watatttatt	tcattaattt	ctttcctkgt	ttacgtwaat	tttgaaaaga	wtgcatgatt	480
tcttgacaga	aatcgatctt	gatgctgtgg	aagtagtttg	accacatcc	ctatgagttt	540
ttcttagaat	gtataaaggt	tgtagcccat	cnaacttcaa	agaaaaaat	gaccacatac	600
tttgcaatca	ggctgaaatg	tggcatgctn	ttctaattcc	aactttataa	actagcaaan	660
aagtg						665

<210> 197

<211> 492

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(492)

<223> n = A,T,C or G

<400> 197

ttttnttttt	ttttttttgc	aggaaggatt	ccattttattg	tggatgcatt	ttcacaatat	60
atgtttattg	gagcgatcca	ttatcagtga	aaagtatcaa	gtgtttataa	natttttagg	120
aaggcagatt	cacagaacat	gctngtcngc	ttgcagtttt	aoctegtana	gatnacagag	180
aattatagtc	naaccagtaa	acnaggaatt	tacttttcaa	aagattaaat	ccaaactgaa	240
caaaaattcta	ccctgaaact	tactocatcc	aaatattgga	ataanagtca	gcagtgatag	300
attctcttct	gaactttaga	ttttctagaa	aaatatgtaa	tagtgatcag	gaagagctct	360
tgttcaaaaag	tacaacnaag	caatgttccc	ttaccatagg	ccttaattca	aactttgatc	420
catttcactc	ccatcacggg	agtcaatgct	acctgggaca	cttgtatttt	gttcatnctg	480
ancntggctt	aa					492

<210> 198

<211> 478

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(478)

<223> n = A,T,C or G

<400> 198

tttnttttgn	atttcantct	gtannaanta	ttttcattat	gtttattana	aaaatatnaa	60
tgtntccacn	acaaatcatn	ttacntnagt	aagaggccan	ctacattgta	caacatacac	120
tgagtatatt	ttgaaaagga	caagtttaaa	gtanacncat	attgocganc	atanacacatt	180
tatacatggc	ttgattgata	tttagcacag	canaaactga	gtgagttacc	agaaanaaat	240
nataatagtc	aatcngattt	aagatacaaa	acagatccta	tggtacatan	catcntgtag	300
gagttgtggc	tttatgttta	ctgaaagtca	atgcagttcc	tgtacaaaaga	gatggccgta	360
agcattctag	tacctctact	ccatgggtta	gaatcgtaca	cttatgttta	catatgtnc	420

gggtaagaat tgtgttaagt naanttattgg agagggtccan gagaaaaatt tgatncaa 478

<210> 199
 <211> 482
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(482)
 <223> n = A,T,C or G

<400> 199
 agtgacttgt cctccaacaa aaccccttga tcaagtttgt ggcactgaca atcagacctta 60
 tgctagtacc tgtcatctat tcgctactaa atgcagactg gagggggacca aaaaggggca 120
 tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga 180
 agtgattcag tttcctctac ggatgagaga ctgggtcaag aatatacctca tgcagcttta 240
 tgaagccnac tctgaacacg ctggttatct nagatgagaa ncagagaaat aaagtcnaga 300
 aaatttacct ggangaaaag aggccttngg ctggggacca tcccattgaa ccttctctta 360
 anggacttta agaanaaact accacatgtn tgtngtatcc tgggtgccngg ccgtttantg 420
 aacntngacn ncacccttnt ggaatanant cttgacngcn tcctgaactt gtcctctctgc 480
 ga 482

<210> 200
 <211> 270
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(270)
 <223> n = A,T,C or G

<400> 200
 cggccgcaag tgcaactcca gctggggcgg tgccggacgaa gattctgcca gcagttgggc 60
 cgactgcgac gacggcggcg gcgacagtcg cagggtgcagc gcgggcccct ggggtcttgc 120
 aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gaccttgacg ccgtcgggga 180
 cagccggaac agagcccggt gaangcggga ggcctcgggg agcccctcgg gaagggcggc 240
 ccgagagata cgcaggtgca ggtggccgcc 270

<210> 201
 <211> 419
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(419)
 <223> n = A,T,C or G

<400> 201
 tttttttttt ttttggaaac tactgagagc acagcaggtc agcaacaagt ttattttgca 60
 gctagcaagg taacagggtg gggcatggtt acatgttcag gtcaacttcc tttgtcgtgg 120
 ttgattgggt tgtctttatg ggggcggggt ggggtagggg aaancgaagc anaantaaca 180
 tggagtgggt gcaccctccc tgtagaacct ggttacnaaa gcttggggca gttcacctgg 240

tctgtgaccg	tcattttctt	gacatcaatg	ttattagaag	tcaggatata	tttttagagag	300
tccactgtnt	ctggaggagg	attagggttt	cttgccaana	tccaancaaa	atccacntga	360
aaaagttaga	tgatncangt	acngaatacc	ganggcatan	ttctcatant	cggtggcca	419

<210> 202
 <211> 509
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (509)
 <223> n = A,T,C or G

<400> 202	
tttntttttt	60
tggcacttaa	120
gtnattttnc	180
tacncncaaa	240
aatatatacg	300
ggaactaaaa	360
caacancnnc	420
ggatcttaac	480
caatggnaat	509

<210> 203
 <211> 583
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (583)
 <223> n = A,T,C or G

<400> 203	
tttttttttt	60
tacacatatt	120
taaatggaaa	180
gaaaatcttc	240
atttttcttg	300
gcttctctag	360
agggaaaaca	420
tacgttaata	480
tccatttttag	540
attcaaaagc	583

<210> 204
 <211> 589
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (589)

<223> n = A,T,C or G

<400> 204

ttttttttnt	tttttttttt	tttttttctc	ttcttttttt	ttganaatga	ggatcgagtt	60
tttcactctc	tagatagggc	atgaagaaaa	ctcatctttc	cagcttttaa	ataacaatca	120
aatctcttat	gctatatcat	attttaagtt	aaactaatga	gtcactggct	tatcttctcc	180
tgaaggaaat	ctgttcattc	ttctcattca	tatagttata	tcaagtacta	ccttgcatat	240
tgagaggttt	ttcttctcta	tttacacata	tatttccatg	tgaatttgta	tcaaaccttt	300
attttcatgc	aaactagaaa	ataatgtntt	cttttgcata	agagaagaga	acaatatnag	360
cattacaaaa	ctgctcaaat	tgtttggtta	gnttatccat	tataattagt	tnggcaggag	420
ctaatacaaa	tcacattttac	ngacnagcaa	taataaaaact	gaagtaccag	ttaaatatcc	480
aaaataatta	aaggaacatt	tttagcctgg	gtataattag	ctaattcact	ttacaagcat	540
ttattnagaa	tgaattcaca	tgttattatt	ccntagccca	acacaatgg		589

<210> 205

<211> 545

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(545)

<223> n = A,T,C or G

<400> 205

tttttntttt	ttttttcagt	aataatcaga	acaatattta	tttttatatt	taaaattcat	60
agaaaagtgc	cttacattta	ataaaaagttt	gtttctcaaa	gtgatcagag	gaattagata	120
tngtcttgaa	caccaatatt	aatttgagga	aaatacacca	aaatacatta	agtaaattat	180
ttaagatcat	agagcttgta	agtgaaaaga	taaaatttga	cctcagaaac	tctgagcatt	240
aaaaatccac	tattagcaaa	taaattacta	tggacttctt	gctttaattt	tgtgatgaat	300
atgggggtgc	actggtaaac	caacacattc	tgaaggatac	attacttagt	gatagattct	360
tatgtacttt	gctanatnac	gtggatatga	gttgacaagt	ttctctttct	tcaatctttt	420
aaggggcnag	ngaaatgagg	aagaaaagaa	aaggattacg	catactgttc	tttctatngg	480
aaggattaga	tatgtttcct	ttgccaatat	taaaaaata	ataatgttta	ctactagtga	540
aacc						545

<210> 206

<211> 487

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(487)

<223> n = A,T,C or G

<400> 206

tttttttttt	ttttttagtc	aagtttctna	tttttattat	aattaaagtc	ttggtcattt	60
catttattag	ctctgcaact	tacatattta	aattaaagaa	acgttnttag	acaactgtna	120
caatttataa	atgtaagggt	ccattattga	gtanatatat	tcctccaaga	gtggatgtgt	180
cccttctccc	accaactaat	gaancagcaa	cattagttta	attttattag	tagatnatac	240
actgctgcaa	acgctaattc	tcttctccat	ccccatgtn	atattgtgta	tatgtgtgag	300
ttggtnagaa	tgcatcanca	atctnacaat	caacagcaag	atgaagctag	gcntgggctt	360
tcggtgaaaa	tagactgtgt	ctgtctgaat	caaatgatct	gacctatcct	cggtggcaag	420
aactcttcga	accgcttcct	caaaggcngc	tgccacattt	gtggcntctn	ttgcacttgt	480

ttcaaaa

487

<210> 207
 <211> 332
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(332)
 <223> n = A,T,C or G

<400> 207
 tgaattggct aaaagactgc atttttanaa ctagcaactc ttatttcttt cctttaaaaa 60
 tacatagcat taaatcccaa atcctattta aagacctgac agcttgagaa ggctcactact 120
 gcatttatag gaccttctgg tggttctgct gttacnttg aantctgaca atccttgana 180
 atctttgcat gcagaggagg taaaagggtat tggattttca cagaggaana acacagcgca 240
 gaaatgaagg ggccaggctt actgagcttg tccactggag ggctcatggg tgggacatgg 300
 aaaagaaggc agcctaggcc ctggggagcc ca 332

<210> 208
 <211> 524
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(524)
 <223> n = A,T,C or G

<400> 208
 agggcggtgt gcggaggggc ttactgtttt gtctcagtaa caataaatac aaaaagactg 60
 gttgtgttcc ggccccatcc aaccacgaag ttgatttctc ttgtgtgcag agtgactgat 120
 tttaaaggac atggagcttg tcacaatgtc acaatgtcac agtgtgaagg gcacactcac 180
 tccccggtga ttcacattta gcaaccaaca atagctcatg agtccatact tgtaaatact 240
 tttggcagaa tacttnttga aacttgcaga tgataactaa gatocaagat atttcccaaa 300
 gtaaatagaa gtgggtcata atattaatta cctgttcaca tcagcttcca tttacaagtc 360
 atgagcocag acactgacat caaactaagc ccacttagac tcttcaccac cagtctgtcc 420
 tgatcatcaga caggaggctg tcaccttgac caaattctca ccagtcaatc atctatocaa 480
 aaaccattac ctgatccact tccggtaatg caacccttg gtga 524

<210> 209
 <211> 159
 <212> DNA
 <213> Homo sapien

<400> 209
 ggggtgaggaa atccagagtt gccatggaga aaattocagt gtcagcattc ttgctccttg 60
 tggccctctc ctacactctg gcagagata ccacagtcaa acctggagcc aaaaaggaca 120
 caaaggactc tcgacccaaa ctgccccaga cctctctca 159

<210> 210
 <211> 256
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(256)
 <223> n = A,T,C or G

<400> 210
 actccctggc agacaaaggc agaggagaga gctctgtag ttctgtgtg ttgaactgcc 60
 actgaatttc tttccacttg gactattaca tgccanttga gggactaatg gaaaaacgta 120
 tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat 180
 ttgcagggtg naaatgggan ggctgggttg ttanatgaac agggacatag gaggtaggca 240
 ccaggatgct aaatca 256

<210> 211
 <211> 264
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(264)
 <223> n = A,T,C or G

<400> 211
 acattgtttt ttgagataa agcattgaga gagctctct taacgtgaca caatggaagg 60
 actggaacac ataccacat cttgttctg agggataatt ttctgataaa gtcttgctgt 120
 atattcaagc acatatgta tatattattc agttccatgt ttatagccta gttaaggaga 180
 ggggagatac attcngaaag aggactgaaa gaaatactca agtnggaaaa cagaaaaaga 240
 aaaaaaggag caaatgagaa gcct 264

<210> 212
 <211> 328
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(328)
 <223> n = A,T,C or G

<400> 212
 acccaaaaat ccaatgctga atatttggct tcattattcc canattcttt gattgtcaaa 60
 ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag 120
 gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccgccag 180
 ttnaatttca ttccattga cttgggatcc ttatcatcag ccagagagat tgaaaattta 240
 cccctacnac tctttactct ctgganaggg ccagtgggtg tagctataag cttggccaca 300
 ttttttttct cttttattct ttgtcaga 328

<210> 213
 <211> 250
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1) ... (250)

<223> n = A,T,C or G

<400> 213

acttatgagc agagcgacat atccnagtgt agactgaata aaactgaatt ctctccagtt	60
taaagcattg ctactgaag ggatagaagt gactgccagg agggaaagta agccaaggct	120
cattatgccca aagganatat acatttcaat tctccaaact tcttctcat tccaagagtt	180
ttcaatatatt gcatgaacct gctgataanc catgttaana aacaaatata tctctnacct	240
tctcatcggt	250

<210> 214

<211> 444

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (444)

<223> n = A,T,C or G

<400> 214

accagaatc caatgctgaa tatttggtt cattattccc agattctttg attgtcaaag	60
gatttaattg tgtctcagct tgggcacttc agttaggacc taaggatgcc agccggcagg	120
tttatatatg cagcaacaat attcaagcgc gacaacaggt tattgaactt gcccgccagt	180
tgaatttcat tcccattgac ttgggatacct tatcatcagc canagagatt gaaaatttac	240
ccctacgact ctttactctc tggagagggc cagtgggtgt agctataagc ttggccacat	300
ttttttttcc tttattcctt tgtcagagat gcgattcatc catatgctan aaaccaacag	360
agtgactttt acaaaattcc tataganatt gtgaataaaa ccttacctat agttgccatt	420
actttgctct ccctaataata cctc	444

<210> 215

<211> 366

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (366)

<223> n = A,T,C or G

<400> 215

acttatgagc agagcgacat atccaagtgt anaactgaata aaactgaatt ctctocagtt	60
taaagcattg ctactgaag ggatagaagt gactgccagg agggaaagta agccaaggct	120
cattatgccca aagganatat acatttcaat tctccaaact tcttctcat tccaagagtt	180
ttcaatatatt gcatgaacct gctgataagc catgttgaga aacaaatata tctctgacct	240
tctcatcggt aagcagaggc tgtaggcaac atggaocata gcgaanaaaa aacttagtaa	300
tccaagctgt tttctacact gtaacaggt ttccaaccaa ggtggaaatc tctataactt	360
ggtgcc	366

<210> 216

<211> 260

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(260)

<223> n = A,T,C or G

<400> 216

ctgtataaac	agaactccac	tgcangaggg	agggccgggc	caggagaatc	tccgcttgtc	60
caagacaggg	gcctaaggag	ggtctccaca	ctgctnntaa	gggctnttnc	atttttttat	120
taataaaaag	tnnaaaaggc	ctctttctca	cttttttccc	ttnggctgga	aaatttaaaa	180
atcaaaaatt	tcctnaagtt	ntcaagctat	catatatact	ntatcctgaa	aaagcaacat	240
aattcttcct	tcctctctt					260

<210> 217

<211> 262

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(262)

<223> n = A,T,C or G

<400> 217

acctacgtgg	gtaagtttan	aaatgttata	atttcaggaa	naggaacgca	tataattgta	60
tcttgccctat	aattttctat	tttaataagg	aaatagcaaa	ttgggggtggg	gggaatgtag	120
ggcattctac	agtttgagca	aaatgcaatt	aaatgtggaa	ggacagcact	gaaaaatttt	180
atgaataatc	tgtatgatta	tatgtctcta	gagtagattt	ataattagcc	acttacccta	240
atatacttca	tgcttgtaaa	gt				262

<210> 218

<211> 205

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(205)

<223> n = A,T,C or G

<400> 218

accaaggtgg	tgcattaccg	gaantggatc	aangacacca	tcgtggccaa	cccctgagca	60
cccctatcaa	ctcccctttg	tagtaaaactt	ggaaccttgg	aaatgaccag	gccaaagactc	120
aggcctcccc	agttctactg	acctttgtcc	ttangtntna	ngtccagggt	tgctaggaaa	180
anaaatcagc	agacacaggt	gtaaa				205

<210> 219

<211> 114

<212> DNA

<213> Homo sapien

<400> 219

tactgttttg	tctcagtaac	aataaatata	aaaagactgg	ttgtgttccg	gccccatcca	60
accacgaagt	tgatttctct	tgtgtgcaga	gtgactgatt	ttaaaggaca	tgga	114

<210> 220

<211> 93

<212> DNA

<213> Homo sapien

<400> 220

actagccagc	acaaaaggca	gggtagcctg	aattgcttcc	tgctctttac	atttctttta	60
aaataagcat	ttagtgctca	gtccctactg	agt			93

<210> 221

<211> 167

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (167)

<223> n = A,T,C or G

<400> 221

actangtgca	gggtgcgcaca	aatatttgtc	gatattccct	tcattcttga	ttccatgagg	60
tcttttgccc	agcctgtggc	tctactgtag	taagtttctg	ctgatgagga	gccagnatgc	120
ccccactac	cttccctgac	gctccccana	aatcacccaa	cctctgt		167

<210> 222

<211> 351

<212> DNA

<213> Homo sapien

<400> 222

agggcgtggt	gcggagggcg	gtactgacct	cattagtagg	aggatgcatt	ctggcacccc	60
gttcttcacc	tgtcccccaa	tccttaaaaag	gccatactgc	ataaagtcaa	caacagataa	120
atgtttgctg	aattaaagga	tggatgaaaa	aaattaataa	tgaatttttg	cataatccaa	180
ttttctcttt	tatatttcta	gaagaagttt	ctttgagcct	attagatccc	gggaatcttt	240
taggtgagca	tgattagaga	gcttgtaggt	tgcttttaca	tatatctggc	atatttgagt	300
ctcgtatcaa	aacaatagat	tggtaaaggt	ggtattattg	tattgataag	t	351

<210> 223

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (383)

<223> n = A,T,C or G

<400> 223

aaaacaaaca	aacaaaaaaa	acaattcttc	attcagaaaa	attatcttag	ggactgatat	60
tggttaattat	ggtcaattta	atwrtttkt	ggggcatttc	cttacattgt	cttgacaaga	120
ttaaaatgtc	tgtgccaaaa	ttttgtattt	tatttggaga	cttcttatca	aaagtaatgc	180
tgccaaagga	agtctaagga	attagtagtg	ttcccmtcac	ttgtttggag	tgtgctattc	240
taaaagattt	tgatttcctg	gaatgacaat	tatattttta	ctttgggtggg	ggaaanagtt	300
ataggaccac	agtctttract	tctgatactt	gtaaaattaat	cttttattgc	acttgttttg	360
accattaagc	tatatgttta	aaa				383

<210> 224

<211> 320
 <212> DNA
 <213> Homo sapien

<400> 224
 cccctgaagg cttcttggtta gaaaatagta cagttacaac caataggaac aacaaaaaga 60
 aaaagtttgt gacattgttag tagggagtgt gtacccttta ctcccatca aaaaaaaat 120
 ggatacatgg ttaaaggata raagggaat attttatcat atgttctaaa agagaaggaa 180
 gagaaaatac tactttctcr aaatggaagc ccttaaaggt gctttgatac tgaaggacac 240
 aaatgtggcc gtccatcctc ctttaragtt gcatgacttg gacacggtaa ctgttgacgt 300
 tttaractcm gcattgtgac 320

<210> 225
 <211> 1214
 <212> DNA
 <213> Homo sapien

<400> 225
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 ttctgctcgg gcgtcctggt gcatccgcag tgggtgctgt cagccgcaca ctgtttccag 120
 aactcctaca ccatcggggt gggcctgcac agtcttgagg ccgaccaaga gccagggagc 180
 cagatggtgg aggccagcct ctccgtacgg caccagagt acaacagacc ctgtctcgct 240
 aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtctgacac catccggagc 300
 atcagcattg cttcgacgtg ccctaccgcg gggaaactctt gcctcgtttc tggctggggg 360
 ctgctggcga acggcagaat gcctaccgtg ctgcagtgcg tgaacgtgtc ggtggtgtct 420
 gaggaggtct gcagtaagct ctatgacccg ctgtaccacc ccagcatgtt ctgcgcgggc 480
 ggagggcaag accagaagga ctctgcaac ggtgactctg gggggccctt gatctgcaac 540
 ggggtacttg agggccttgt gtctttcgga aaagccccgt gtggccaagt tggcgtgcca 600
 ggtgtctaca ccaacctctg caaattcact gagtggatag agaaaaccgt ccaggccagt 660
 taactctggg gactgggaac ccatgaaatt gacccccaaa tacatcctgc ggaagggaatt 720
 caggaatatc tggtcccagc cctcctccc tcaggcccag gagtccaggc cccagcccc 780
 tctcctcctca aaccaagggt acagatcccc agccccctc ctctcagacc caggagtcca 840
 gacccccag cccctcctcc ctccagacca ggagtccagc ccctcctccc tcagaccag 900
 gagtccagac cccccagccc ctctcctc agacccagggt gtccaggccc ccaaccctc 960
 ctccctcaga ctccagagtc caagocccca accctcctt cccagaccc agaggtccag 1020
 gtcccagccc ctctcctc agacccagcg gtccaatgcc acctagactc tccctgtaca 1080
 cagtgcctcc ttgtggcacg ttgacccaac cttaccagtt ggtttttcat ttttgtccc 1140
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 aaaaaaaaaa aaaa 1214

<210> 226
 <211> 119
 <212> DNA
 <213> Homo sapien

<400> 226
 acccagtatg tgcagggaga cggaacccca tgtgacagcc cactccacca gggttcccaa 60
 agaacctggc ccagtcataa tcattcatcc tgacagtggc aataatcacg ataaccagt 119

<210> 227
 <211> 818
 <212> DNA
 <213> Homo sapien

<400> 227

acaattcata	gggacgacca	atgaggacag	ggaatgaacc	cggtctctcc	ccagccctga	60
tttttgctac	atatggggtc	ccttttcatt	ctttgcaaaa	acactgggtt	ttctgagaac	120
acggacgggt	cttagcacia	tttgtgaaat	ctgtgtaraa	ccgggctttg	caggggagat	180
aattttctct	ctctggagga	aaggtgggtga	ttgacaggca	gggagacagt	gacaaggcta	240
gagaaagcca	cgctcggcct	tctctgaacc	aggatggaac	ggcagacccc	tgaaaacgaa	300
gcttgtcccc	ttccaatcag	ccacttctga	gaacccccat	ctaacttcct	actggaaaag	360
agggcctcct	caggagcagt	ccaagagttt	*tcaaagataa	cgtgacaact	accatctaga	420
ggaaaggggtg	caccctcagc	agagaagccg	agagcttaac	tctggtcgtt	tctagagaca	480
acctgctggc	tgtcttgagg	tgcgcccagc	ctttgagagg	ccactacccc	atgaacttct	540
gccatccact	ggacatgaag	ctgaggacac	tgggcttcaa	cactgagttg	tcatgagagg	600
gacaggctct	gccctcaagc	cggttgaggg	cagcaaccac	tctcctcccc	tttctcacgc	660
aaagccattc	ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagtttggtc	720
caagaggata	tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct	aggttttcag	cctagatggg	agtcgtgt			818

<210> 228

<211> 744

<212> DNA

<213> Homo sapien

<400> 228

actggagaca	ctgttgaact	tgatcaagac	ccagaccacc	ccaggtctcc	ttcgtgggat	60
gtcatgacgt	ttgacatacc	tttggaaacga	gcctcctcct	tggagatgg	aagaccgtgt	120
tcgtggccga	cctggcctct	cctggcctgt	ttcttaagat	gcggagtcac	atttcaatgg	180
taggaaaagt	ggcttcgtaa	aatagaagag	cagtcactgt	ggaactacca	aatggcgaga	240
tgtctgggtc	acattggggg	gctttgggat	aaaagattta	tgagccaact	attctctggc	300
accagattct	aggccagttt	gttccactga	agcttttccc	acagcagtc	acctctgcag	360
gctggcagct	gaatggcttg	ccggtggctc	tgtggcaaga	tcacactgag	atcgatgggt	420
gagaaggcta	ggatgcttgt	ctagtgttct	tagctgtcac	gttggctcct	tccaggttgg	480
ccagacgggtg	ttggccactc	ccttctaaaa	cacaggcgcc	ctcctgggtga	cagtgacccg	540
ccgtgggatg	ccttggccca	ttccagcagt	ccagttatg	catttcaagt	ttgggggtttg	600
ttcttttctg	taatgttctt	ctgtgttctc	agctgtcttc	atttcctggg	ctaagcagca	660
ttgggagatg	tggaaocagag	atccactcct	taagaaccag	tggcgaaaga	caotttcttt	720
cttcactctg	aagtagctgg	tggg				744

<210> 229

<211> 300

<212> DNA

<213> Homo sapien

<400> 229

cgagtctggg	ttttgtctat	aaagtttgat	ccctcctttt	ctcatocaaa	tcattgtgaac	60
cattacacat	cgaaataaaa	gaaagggtggc	agacttgccc	aacgocaggc	tgacatgtgc	120
tgcagggttg	ttgtttttta	attattattg	ttagaaacgt	caocacagct	ccctgttaat	180
ttgtatgtga	cagocaaactc	tgagaagggtc	ctatttttcc	acctgcagag	gatocagttc	240
cactaggctc	ctccttgccc	tcacactgga	gtctccgcca	gtgtgggtgc	ccactgacat	300

<210> 230

<211> 301

<212> DNA

<213> Homo sapien

<400> 230

cagcagaaca	aatacaaaata	tgaagagtgc	aaagatctca	taaaatctat	gctgaggaat	60
gagcgacagt	tcaaggagga	gaagcttgca	gagcagctca	agcaagctga	ggagctcagg	120

caatataaag	tcctggttca	cactcaggaa	cgagagctga	cccagttaag	ggagaagttg	180
cggaagggga	gagatgcctc	cctctcattg	aatgagcatc	tccaggccct	cctcactccg	240
gatgaaccgg	acaagtccca	ggggcaggac	ctccaagaaa	cagacctcgg	ccgcgaccac	300
g						301

<210> 231

<211> 301

<212> DNA

<213> Homo sapien

<400> 231

gcaagcacgc	tggaacatct	ctgtcaggtc	agctccagag	aagccattag	tcatttttagc	60
caggaactcc	aagtccacat	ccttggcaac	tggggacttg	cgcagggttag	ccttgaggat	120
ggcaacacgg	gactttctcat	caggaagtgg	gatgtagatg	agctgatcaa	gacggccagg	180
tctgaggatg	gcaggatcaa	tgatgtcagg	ccggttggtg	ccgccaatga	tgaacacatt	240
tttttttg	gacatgccat	ccattttctgt	caggatctgg	ttgatgactc	ggtcagcagc	300
c						301

<210> 232

<211> 301

<212> DNA

<213> Homo sapien

<400> 232

agtaggtatt	tcgtgagaag	ttcaacacca	aaactggaac	atagttctcc	ttcaagtgtt	60
ggcgacagcg	gggcttcctg	attctggaat	ataactttgt	gtaaattaac	agccacctat	120
agaagagtcc	atctgctgtg	aaggagagac	agagaactct	gggttccgtc	gtcctgtcca	180
cgtgctgtac	caagtgtctg	tgccagcctg	ttacctgttc	tactgaaaa	tctggctaatt	240
gctcttgtgt	atcactttctg	attctgacaa	tcaatcaatc	aatggcctag	agcactgact	300
g						301

<210> 233

<211> 301

<212> DNA

<213> Homo sapien

<400> 233

atgactgact	tcccagtaag	gctctctaag	gggtaagtag	gaggatccac	aggatttgag	60
atgctaaggc	cccagagatc	gtttgatcca	accctcttat	tttcagaggg	gaaaaatggg	120
cctagaagtt	acagagcatc	tagctgggtc	gctggcacc	ctggcctcac	acagactccc	180
gagtagctgg	gactacaggc	acacagtcac	tgaagcaggc	cctgttagca	attctatgcg	240
tacaaattaa	catgagatga	gtagagactt	tattgagaaa	gcaagagaaa	atcctatcaa	300
c						301

<210> 234

<211> 301

<212> DNA

<213> Homo sapien

<400> 234

aggctctaca	catcgagact	catccatgat	tgatatgaat	ttaaaaatta	caagcaaaga	60
cattttattc	atcatgatgc	tttcttttgt	ttcttctttt	cgttttcttc	tttttctttt	120
tcaatttcag	caacatactt	ctcaaattct	tcaggattta	aaatcttgag	ggattgatct	180
cgcctcatga	cagcaagttc	aatgtttttg	ccactgact	gaaccacttc	caggagtgcc	240
ttgatcacca	gcttaatggt	cagatcatct	gcttcaatgg	cttcgtcagt	atagttcttc	300

t

301

<210> 235
 <211> 283
 <212> DNA
 <213> Homo sapien

<400> 235
 tggggctgtg catcaggcgg gtttgagaaa tattcaattc tcagcagaag ccagaatttg 60
 aattccctca tcttttaggg aatcatttac caggtttggg gaggattcag acagctcagg 120
 tgctttcact aatgtctctg aacttctgtc octctttgtt catggatagt ccaataaata 180
 atgttatctt tgaactgatg ctcataggag agaataaag aactctgagt gatatcaaca 240
 ttagggattc aaagaaatat tagatttaag ctcacactgg tca 283

<210> 236
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 236
 aggtcctcca ccaactgcct gaagcacggt taaaattggg aagaagtata gtgcagcata 60
 aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg 120
 tcggagcagc atcattaata ccaagcagaa tgcgtaatat ataaatacaa tggatatag 180
 tgggtagacg gcttcatgag tacagtgtac tgggtatcg taatctggac ttgggttgta 240
 aagcatcgtg taccagtcag aaagcatcaa tactcgacat gaacgaatat aaagaacacc 300
 a 301

<210> 237
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 237
 cagtggtagt ggtgggtggac gtggcggttg tctgtgtgcc ttttttgggtg ccggtcacia 60
 actcaatttt tgttcgctcc tttttggcct ttccaattt gtocatctca attttctggg 120
 ccttggtcaa tgctcatag taggagtoct cagaccagcc atggggatca aacataatct 180
 ttgggtagtt ggtgccaaagc tctgcaatgg cacagaatgg atcagcttct cgtaaatcta 240
 gggttccgaa attctttctt cctttgggata atgtagttca tatocattcc ctcttttacc 300
 t 301

<210> 238
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 238
 gggcagggttt tttttttttt ttttttgatg gtgcagaccc ttgctttatt tgtctgactt 60
 gttcacagtt cagcccccctg ctcaaaaaac caacggggcca gctaaggaga ggaggaggca 120
 ccttgagact tccggagtcg aggtctctca ggggttcccc gccatcaat cattttctgc 180
 acccccctgcc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggattcca 240
 gtgtgggacc cagggtctgt tcttcacagt agggagtgga agggatgact aatttcttta 300
 t 301

<210> 239
 <211> 239

<212> DNA

<213> Homo sapien

<400> 239

ataagcagct aggggaattct ttatttagta atgtcctaac ataaaagttc acataactgc	60
ttctgtcaaa ccatgatact gagctttgtg acaaccaga aataactaag agaaggcaaa	120
cataatacct tagagatcaa gaaacattta cacagttcaa ctgtttaaaa atagctcaac	180
attcagccag tgagtagagt gtgaatgcc a gcatacacag tatacaggtc cttcagggg	239

<210> 240

<211> 300

<212> DNA

<213> Homo sapien

<400> 240

ggtcctaatag aagcagcagc ttccacattt taacgcaggt ttacgggtgat actgtccttt	60
gggatctgcc ctccagtggg accttttaag gaagaagtgg gcccaagcta agttccacat	120
gctgggtgag ccagatgact tctgttcctt ggtaactttt ttcaatgggg cgaatggggg	180
ctgccaggtt tttaaaatca tgcttcattt tgaagcacac ggtaacttca cctcctcac	240
gctgtgggtg tactttgatg aaaataccca ctttgttggc ctttctgaag ctataatgtc	300

<210> 241

<211> 301

<212> DNA

<213> Homo sapien

<400> 241

gaggtctggt gctgaggtct ctgggctagg aagaggagtt ctgtggagct ggaagccaga	60
cctctttgga ggaaactcca gcagctatgt tgggtgtctct gaggggaatgc aacaaggctg	120
ctcctccatg tattggaaaa ctgcaaaactg gactcaactg gaaggaagtg ctgctgccag	180
tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct	240
tcctcctcct gtcatacggg ctctctcaag catcctttgt tgtcaggggc ctaaaaggga	300
g	301

<210> 242

<211> 301

<212> DNA

<213> Homo sapien

<400> 242

ccgagggtcct gggatgcaac caatcactct gtttcacgtg acttttatca ccatacaatt	60
tgtggcattt cctcattttc tacattgtag aatcaagagt gtaaataaat gtatatcgat	120
gtcttcaaga atatatcatt cttttttcac tagaaccat tcaaaatata agtcaagaat	180
cttaatatca acaaatatat caagcaaact ggaaggcaga ataactacca taatttagta	240
taagtaccca aagttttata aatcaaaagc cctaatagata accattttta gaattcaatc	300
a	301

<210> 243

<211> 301

<212> DNA

<213> Homo sapien

<400> 243

aggtaagtc cagtttgaag ctcaaaagat ctggtatgag cataggctca tcgacgacat	60
ggtggcccaa gctatgaaat cagagggagg cttcatctgg gcctgtaaaa actatgatgg	120

tgacgtgcag tcggactctg tggcccaagg gstatggctct ctccggcatga tgaccagcgt 180
 gctgggttgt ccagatggca agacagtaga agcagaggct gccacggga ctgtaacccg 240
 tcaactaccgc atgttcaga aaggacagga gacgtccacc aatccattg ctccatttt 300
 t 301

<210> 244
 <211> 300
 <212> DNA
 <213> Homo sapien

<400> 244
 gctgggttgc aagaatgaaa tgaatgattc tacagctagg acttaacctt gaaatggaaa 60
 gtcattgcaat ccattttgca ggatctgtct gtgcacatgc ctctgtagag agcagcattc 120
 ccagggacct tggaaacagt tgacactgta aggtgcttgc tccccaagac acatccataa 180
 aggtgttgta atgggtgaaa cgtcttcctt ctttattgcc ccttcttatt tatgtgaaca 240
 actgtttgtc ttttgtgtat cttttttaa ctgtaaagt caattgtgaa aatgaatatc 300

<210> 245
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 245
 gtctgagtat taaaaatgtt attgaaatta tccccaacca atgttagaaa agaaagagg 60
 tatatactta gataaaaaat gaggtgaatt actatccatt gaaatcatgc tcttagaatt 120
 aaggccagga gatattgtca ttaatgtara cttcaggaca ctagagtata gcagccctat 180
 gttttcaaag agcagagatg caattaaata ttgttttagca tcaaaaaggc cactcaatac 240
 agctaataaa atgaaagacc taattttctaa agcaattctt tataattttac aaagttttaa 300
 g 301

<210> 246
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 246
 ggtctgtcct acaatgcctg cttcttgaaa gaagtggca ctttctagaa tagctaaata 60
 acctgggctt attttaaaga actatttgta gtcagattg gtttctctat ggctaaaata 120
 agtgcttctt gtgaaaatta aataaaacag ttaattcaaa gccttgatat atgttaccac 180
 taacaatcat actaaatata ttttgaagta caaagtttga catgctctaa agtgacaacc 240
 caaatgtgtc ttacaaaaca cgttcttaac aaggtatgct ttacactacc aatgcagaaa 300
 c 301

<210> 247
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 247
 aggtcctttg gcagggtcra tggatcagag ctcaaactgg agggaaaggc atttcgggta 60
 gcctaagagg gcgactggcg gcagcacaac caaggaaggc aagggtgttt cccocacgct 120
 gtgtcctgtg ttcagggtgcg acacacaatc ctcatgggaa caggatcacc catgcgctgc 180
 ccttgatgat caagggtggg gcttaagtgg attaaggag gcaagttctg gggtccttgc 240
 cttttcaaac catgaagta ggctctgtat cctcctttt cctaactgat attctaacta 300
 a 301

<210> 248
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 248
 aggtccttgg agatgccatt tcagccgaag gactcttctw ttcggaagta caccctcact 60
 attaggaaga ttcttagggg taatttttct gaggaaggag aactagccaa ctaagaatt 120
 acaggaagaa agtggtttgg aagacagcca aagaaataaa agcagattaa attgtatcag 180
 gtacattcca gcctgttggc aactccataa aaacatttca gattttaatc ccgaatttag 240
 ctaatgagac tggatttttg ttttttatgt tgtgtgtcgc agagctaaaa actcagttcc 300
 c 301

<210> 249
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 249
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 ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgccccgcc 120
 ccagggagac acagcagtga ctacagagctg gtcgcacact gtgcctccct cctcaccgcc 180
 catcgtaatg aattattttg aaaattaatt ccaccatcct ttcagattct ggatggaaag 240
 actgaatctt tgactcagaa ttgtttgctg aaaagaatga rgtgacttct ttagtcattt 300
 a 301

<210> 250
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 250
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 cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc 120
 cataagcaca tcagtacttt tctctggctg gaatagtaaa cttaaagtatg gtacatctac 180
 ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta 240
 caataaaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc 300
 a 301

<210> 251
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 251
 gccgaggtcc tacatttggc ccagtttccc cctgcacccct ctccagggcc cctgcctcat 60
 agacaacctc atagagcata ggagaactgg ttgccctggg ggcaggggga ctgtctggat 120
 ggcaggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct 180
 cattgggatc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccgga 240
 cctctggagg ggggcagtgg aatcccagct ccaggacgga tctgtctgaa aagatattct 300
 c 301

<210> 252
 <211> 301

<212> DNA

<213> Homo sapien

<400> 252

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gcaaccaatc actctgtttc acgtgacttt tatcaocata caatttgtgg catttcctca      60
ttttctacat tgtagaatca agagtgtaaa taaatgtata togatgtctt caagaatata      120
tcattccttt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa      180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag taoccaaagt      240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc      300
a                                                                                   301

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<210> 253

<211> 301

<212> DNA

<213> Homo sapien

<400> 253

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ttccctaaga agatgttatt ttgttgggtt ttgttccccc tccatctcga ttctegtacc      60
caactaaaaa aaaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctecttagct      120
tggtctgatt gttttcagac cttaaaatat aaacttgttt cacaagcttt aatccatgtg      180
gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt      240
tccatagtgc ccacagggtg ttccctcacat tttctccata ggaaaatgct ttttcccaag      300
g                                                                                   301

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<210> 254

<211> 301

<212> DNA

<213> Homo sapien

<400> 254

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cgctgcgcct ttcccttggg ggagggggcaa ggocagaggg ggtccaagtg cagcacgagg      60
aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaaatcccc      120
ccaaatctct tcactttacc ctggtggact cctgactgta gaattttttg gttgaaacaa      180
gaaaaaaata aagcttttga cttttcaagg ttgcttaaca ggtactgaaa gactgggctc      240
acttaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc      300
t                                                                                   301

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<210> 255

<211> 302

<212> DNA

<213> Homo sapien

<400> 255

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agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgtct tttattataa      60
attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagtt tgacttggat      120
tgggattttg ttgagttctt caagcatctc ctaataacct caaggggctg agtagggggg      180
aggaaaaagg actggagggt gaatctttat aaaaaacaag agtgattgag gcagattgta      240
aacattatta aaaaaacaaga aacaaacaaa aaaatagaga aaaaaaccac cccaacacac      300
aa                                                                                   302

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<210> 256

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 256

gttccagaaa	acattgaagg	tggtctccca	aagtctaact	agggataccc	cctctagcct	60
aggaccctcc	tcccacacc	tcaatccacc	aaaccatcca	taatgcaccc	agataggccc	120
acccccaaaa	gcctggacac	cttgagcaca	cagttatgac	caggacagac	tcatctctat	180
aggcaaatag	ctgctggcaa	actggcatta	cctggtttgt	ggggatgggg	gggcaagtgt	240
gtggcctctc	ggcctggtta	gcaagaacat	tcagggtagg	cctaagttan	tcgtgttagt	300
t						301

<210> 257

<211> 301

<212> DNA

<213> Homo sapien

<400> 257

gttgtggagg	aactctggct	tgctcattaa	gtcctactga	ttttcactat	cccctgaatt	60
tccccactta	tttttgtctt	tcactatcgc	aggccttaga	agaggctctac	ctgcctccag	120
tcttacctag	tccagtctac	cccctggagt	tagaatggcc	atcctgaagt	gaaaagtaat	180
gtcacattac	tcccttcagt	gatttcttgt	agaagtgcc	atccctgaat	gccaccaaga	240
tcttaatctt	cacatcttta	atcttatctc	tttgactcct	ctttacaccg	gagaaggctc	300
c						301

<210> 258

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 258

cagcagtagt	agatgccgta	tgccagcacg	cccagcactc	ccaggatcag	caccagcacc	60
agggggccag	ccaccaggcg	cagaagcaag	ataaacagta	ggctcaagac	cagagccacc	120
cccagggcaa	caagaatcca	ataccaggac	tgggcaaaat	cttcaaagat	cttaacactg	180
atgtctcggg	cattgaggct	gtcaataana	cgctgatccc	ctgctgtatg	gtgggtgtcat	240
tggtgatccc	tgggagcgcc	ggtggagtaa	cgttgggtcca	tggaagcag	cgcccacaac	300
t						301

<210> 259

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 259

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tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg    60
gtgtcctgaa gtgatttggg cccctgaggg cagacaccta agtaggaatc ccagtgggaa    120
gcaaagccat aaggaagccc aggattcctt gtgacagga agtgggcccag gaaggtctgt    180
tccdgctcac atctcatctg catgcagcac ggaocggatg cgoocactgg gtcttggctt    240
ccctcccatc ttctcaagca gtgtccttgt tgagccattt gcaccccttg ctccagggtg    300
c

```

```

<210> 260
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 260
tttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaaatt aagcaatggt    60
aagggtgtctt aacttgaaaa agattaggag tcaactggtt acaagttata attgaatgaa    120
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaacia caggattaac    180
tagggcaaaa taaataagtg tgtggaagcc ctgataagtg cttataaac agactgattc    240
actgagacat cagtacctgc ccggggcgcc gctcgagccg aattctgcag atatccatca    300
c

```

```

<210> 261
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 261
aaatattcga gcaaactcctg taactaatgt gtctccataa aaggctttga actcagtgaa    60
tctgtctcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaagggt    120
agcaaccaat attccataca attcatcagc aggaaataaa ggctcttcag aagggtcaat    180
ggtgacatcc aatttcttct gataatttag attcctcaca accttctag ttaagtgaag    240
ggcatgatga tcatccaaag ccagtggtc acttactcca gactttctgc aatgaagatc    300
a

```

```

<210> 262
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 262
gaggagagcc tgttacagca ttgttaagca cagaatactc caggagtatt tgtaattgtc    60
tgtgagcttc ttgocgcaag tctctcagaa atttaaaaag atgcaaatec ctgagtcacc    120
cctagacttc ctaaaaccaga tctcttgggg ctggaacctg gcactctgca tttgtaatga    180
gggttttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtgcc    240
catcattacc ccacattat aatgggatag attcagagca gatactctcc agcaaagaat    300
c

```

```

<210> 263
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1) ... (301)
<223> n = A,T,C or G

```

<400> 263

tttagcttgt	ggtaaatgac	tcacaaaact	gatttttaaaa	tcaagttaat	gtgaattttg	60
aaaattacta	cttaatccta	attcacaata	acaatggcat	taaggtttga	cttgagttgg	120
ttcttagtat	tatttatgg	aaataggctc	ttaccacttg	caaataactg	gccacatcat	180
taatgactga	cttcccagta	aggctctcta	aggggtaagt	angaggatcc	acaggatttg	240
agatgctaag	gccccagaga	tcgtttgatc	caaccctctt	attttcagag	gggaaaatgg	300
g						301

<210> 264

<211> 301

<212> DNA

<213> Homo sapien

<400> 264

aaagacgtta	aaccactcta	ctaccacttg	tggaactctc	aaagggtaaa	tgacaaascc	60
aatgaatgac	tctaaaaaca	atattttacat	ttaatggttt	gtagacaata	aaaaaacaag	120
gtggatagat	ctagaattgt	aacattttta	gaaaaccata	scatttgaca	gatgagaaaag	180
ctcaattata	gatgcaaagt	tataactaaa	ctactatagt	agtaaagaaa	tacatttcac	240
acccttcata	taaattcact	atcttggctt	gaggcactcc	ataaaatgta	tcacgtgcat	300
a						301

<210> 265

<211> 301

<212> DNA

<213> Homo sapien

<400> 265

tgccccaggt	atgtgtaagt	gtatccgcac	ccagaggtaa	aactacactg	tcctctttgt	60
cttcttgtga	cgcagtattt	cttctctggg	gagaagccgg	gaagtcttct	cctggctcta	120
catattcttg	gaagtctcta	atcaactttt	gttccatttg	tttcatttct	tcaggaggga	180
ttttcagttt	gtcaacatgt	tctctaacaa	cacttgccca	tttctgtaaa	gaatccaaag	240
cagtccaagg	ctttgacatg	tcaacaacca	gcataactag	agtatccttc	agagatacgg	300
c						301

<210> 266

<211> 301

<212> DNA

<213> Homo sapien

<400> 266

taccgtctgc	ccttctctcc	atccaggcca	tctgcgaatc	tacatgggtc	ctcctattcg	60
acaccagatc	actctttcct	ctacccacag	gcttgctatg	agcaagagac	acaacctcct	120
ctcttctgtg	ttccagcttc	ttttcctgtt	cttcccaccc	cttaagttct	attcctgggg	180
atagagacac	caatacccat	aacctctctc	ctaagcctcc	ttataacca	gggtgcacag	240
cacagactcc	tgacaactgg	taaggccaat	gaactgggag	ctcacagctg	gctgtgcctg	300
a						301

<210> 267

<211> 301

<212> DNA

<213> Homo sapien

<400> 267

aaagagcaca	ggccagctca	gcctgccctg	gccatctaga	ctcagcctgg	ctccatgggg	60
------------	------------	------------	------------	------------	------------	----

```

gttctcagtg ctgagtcctat ccaggaaaag ctcacctaga ccttctgagg ctgaatcttc      120
atcctcacag gcagcttctg agagcctgat attcctagcc ttgatgggtc ggagtaaagc      180
ctcattctga ttcctctcct tcttttcttt caagttgggt ttcctcacat cctctgttc      240
aattcgcttc agcttgtctg ctttagccct catttocaga agcttcttct ctttggcatc      300
t                                                                                   301

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<210> 268

<211> 301

<212> DNA

<213> Homo sapien

<400> 268

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aatgtctcac tcaactactt cccagcctac cgtggcctaa ttctgggagt tttcttctta      60
gatcttggga gagctgggtc ttctaaggag aaggaggaag gacagatgta actttggatc      120
tcgaagagga agtctaattg aagtaattag tcaacgggtc ttgttttagac tcttgggaata      180
tgctgggtgg ctcagtgagc ccttttggag aaagcaagta ttattcttaa ggagtaacca      240
cttccattg ttctactttc taocatcatc aattgtatat tatgtattct ttggagaact      300
a                                                                                   301

```

<210> 269

<211> 301

<212> DNA

<213> Homo sapien

<400> 269

```

taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat      60
aaaattacct ttattcacac atctcaaaac aattctgcaa attcttagtg aagtttaact      120
atagtcacag accttaaata ttcacattgt tttctatgtc tactgaaaat aagttcacta      180
cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca cccccaatta      240
tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc      300
t                                                                                   301

```

<210> 270

<211> 301

<212> DNA

<213> Homo sapien

<400> 270

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cattgaagag cttttgcgaa acatcagaac acaagtgcct ataaaattaa ttaagcctta      60
cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga      120
gagcttgctg gtgcagtgca tattggataa cactattcat ggocgaattg atcaagtcaa      180
ccaactcctt gaactggatc atcagaagaa ggggtgggtg cgatatactg cactagataa      240
tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggcct aacagaaaac      300
a                                                                                   301

```

<210> 271

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (301)

<223> n = A,T,C or G

<400> 271

aaaaggttct	cataagatta	acaatttaaa	taaatatttg	atagaacatt	ctttctcatt	60
tttatagctc	atcttttagg	ttgatattca	gttcatgctt	cccttgctgt	tcttgatcca	120
gaattgcaat	cacttcatca	gcctgtattc	gtcceaattc	tctataaagt	gggtccaagg	180
tgaaccacag	agccacagca	cacctcttcc	cttggtgac	tgccttcacc	ccatganggt	240
tctctcctcc	agatganaac	tgatcatgcg	cccacatttt	gggttttata	gaagcagtca	300
c						301

<210> 272

<211> 301

<212> DNA

<213> Homo sapien

<400> 272

taaattgcta	agccacagat	aacaccaatc	aaatggaaca	aatcactgtc	ttcaaagtgc	60
ttatcagaaa	accaaagtag	cctggaatct	tcataatacc	taaacatgcc	gtatttagga	120
tccaataatt	ccctcatgat	gagcaagaaa	aattctttgc	gcacccctcc	tgcattccaca	180
gcattcttct	caacaaatat	aaccttgagt	ggcttcttgt	aatctatgtt	ctttgttttc	240
ctaaggactt	ccattgcata	tcctacaata	ttttctctac	gcaccactag	aattaagcag	300
g						301

<210> 273

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 273

acatgtgtgt	atgtgtatct	ttgggaaan	aanaagacat	cttggttayt	atttttttgg	60
agagangctg	ggacatggat	aatcacwtaa	tttgctayta	tyactttaat	ctgactygaa	120
gaaccgtcta	aaaataaaat	ttaccatgtc	dtatattcct	tatagtatgc	ttatttcacc	180
tttcttctgt	ccagagagag	tatcagtgc	ananatttma	gggtgaamac	atgmattggt	240
gggacttnty	tttacngagm	acctgccc	sgcgcctcg	makengantt	ccgcsananc	300
t						301

<210> 274

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 274

cttatatact	ctttctcaga	ggcaaaagag	gagatgggta	atgtagacaa	ttctttgagg	60
aacagtaaat	gattattaga	gagaangaat	ggaccaagga	gacagaaatt	aacttgtaaa	120
tgattctctt	tggaaatctga	atgagatcaa	gaggccagct	ttagcttggtg	gaaaagtcca	180
tctaggtatg	gttgcatctt	cgtcttcttt	tctgcagtag	ataatgaggt	aaccgaaggc	240
aattgtgctt	cttttgataa	gaagctttct	tggtcatatc	aggaaattcc	aganaaagtc	300

c

301

<210> 275
 <211> 301
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 275

tcggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg	60
gggtgaaatt ggccaacttt ctattaactt atgttggcaa ttttggcacc aacagtaagc	120
tggcccttct aataaaagaa aattgaaagg tttctcacta aacggaatta agtagtggag	180
tcaagagact ccaggcctc agcgtacctg cccgggcggc cgctcgaagc cgaattctgc	240
agatatccat cacactggcg gncgctcgan catgcatcta gaaggnocaa ttcgcctat	300
a	301

<210> 276
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 276

tgtacacata ctcaataaat aaatgactgc attgtggtat tattactata ctgattatat	60
ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat	120
taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc	180
caatacatTT aaacatttgg gaaatgaggg ggacaaatgg aagocagatc aaatttgtgt	240
aaaactattc agtatgttcc ccttgcttca tgtctgagaa ggctctcctt caatggggat	300
g	301

<210> 277
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 277

tttgttgatg tcagtatTTT attacttgcg ttatgagtgc tcacotggga aattctaaag	60
atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg	120
gaatcatggc actcctgata ctttcccaa tcaacactct caatgcccc cctcgtctct	180
caccatagtg gggagactaa agtggccacg gatttgccct angtgtgcag tgggttctga	240
gttcnctgtc gattacatct gaecagtctc ctttttcga agtcnctcg tccaatcttg	300
c	301

<210> 278
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 278
 taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60
 aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca 120
 cagtctctac tgttattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180
 aatgaacatc tcatgtgtgc tcacaatggt ctggcactat tataagtgct tcacagggtt 240
 tatgtgttct tcgtaacttt atggantagg tactcggccg cgaacacgct aagccgaatt 300
 c 301

<210> 279
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 279
 aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60
 gttatatata ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120
 ttagaccttt accttcacag caccacacag tgcttgatat ttcagagtca gtcattgggt 180
 atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240
 catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300
 a 301

<210> 280
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 280
 ggtactggag ttttcctccc ctgtgaaaac gtaactactg ttgggagtgat attgaggatg 60
 tagaaagggtg gtggaaccaa attgtgggtca atggaaatag gagaatatgg ttctcactct 120
 tgagaaaaaa acctaaagatt agcccaggta gttgcctgta acttcagttt ttctgcctgg 180
 gtttgatata gtttaggggtt ggggttagat taagatctaa attacatcag gacaaagaga 240
 cagactatta actccacagt taattaagga ggtatgttcc atgtttattt gttaaagcag 300
 t 301

<210> 281
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 281
 aggtacaaga aggggaatgg gaaagagctg ctgctgtggc attgttcaac ttggatatcc 60
 gccgagcaat ccaaatacctg aatgaagggg catcttctga aaaaggagat ctgaatctca 120
 atgtggtagc aatggcttta tcgggttata cggatgagaa gaactccctt tggagagaaa 180
 tgtgtagcac actgcgatta cagctaaata acccgatttt gtgtgtcatg tttgcatttc 240

tgacaagtga aacaggatct tacgatggag ttttgatatga aaacaaagtt gcagtacctc 300
g 301

<210> 282
<211> 301
<212> DNA
<213> Homo sapien

<400> 282
cagggtactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca 60
tccagaacct aaaaattaag aaattcaaaa agacattttg tgggcacctg ctagcacaga 120
agcgacagaag caaagcccag gcagaacctat gctaacctta cagctcagcc tgcacagaag 180
cgcagaagca aagcccaggc agaaccatgc taaccttaca gctcagcctg cacagaagcg 240
cagaagcaaa gccacggcag aacatgctaa ccttacagct cagcctgcac agaagcacag 300
a 301

<210> 283
<211> 301
<212> DNA
<213> Homo sapien

<400> 283
atctgtatac ggcagacaaa ctttatarag tgtagagagg tgagcgaaaag gatgcaaaaag 60
cactttgagg gctttataat aatatgctgc ttgaaaaaaa aaatgtgtag ttgatactca 120
gtgcatctcc agacatagta aggggttgct ctgaccaatc aggtgatcat tttttctatc 180
acttcccagg ttttatgcaa aaattttgtt aaattctata atggtgatat gcattcttta 240
ggaaacatat acatttttaa aaatctattt tatgtaagaa ctgacagacg aatttgcttt 300
g 301

<210> 284
<211> 301
<212> DNA
<213> Homo sapien

<400> 284
caggtaaaa acgctattaa gtggcctaga atttgaacat ttgtggtctt tatttacttt 60
gcttcgtgtg tgggcaaagc aacatcttcc ctaaatatat attaccaaga aaagcaagaa 120
gcagattagg tttttgacaa aacaaacagg ccaaaaagggg gctgaacctg agcagagcat 180
ggtgagaggc aaggcatgag agggcaagtt tggttgaggc agatctgtgc ctactttatt 240
actggagtaa aagaaaacaa agttcattga tgctgaagga tatatacagt gttagaatt 300
a 301

<210> 285
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)... (301)
<223> n = A,T,C or G

<400> 285
acatcaocat gatcgatcc cccacocatt atacgttgta tgcttacata aatactcttc 60
aatgatcatt agtgtcttaa aaaaaatact gaaaactcct tctgcatccc aatctctaac 120

caggaaagca aatgctatTT acagacctgc aagccctccc tcaaacnaaa ctatTTctgg 180
 attaaatatg tctgacttct tttgaggTca cacgactagg caaatgctat ttacgatctg 240
 caaaagctgt ttgaagagtc aaagcccccT tgtgaacacg atttctggac cctgtaacag 300
 t 301

<210> 286
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 286
 taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaaa aaactttgct 60
 tgtatatatt ttttgcttta cagtggatca ttctagtagg aaaggacagt aagatttttt 120
 atcaaaatgt gtcatgccag taagagatgt tatattcttt tctcatttct tccccaccca 180
 aaaataagct accatatagc ttataagtct caaatttttg ctttttacta aaatgtgatt 240
 gtttctgttc attgtgtatg cttcatcacc tatattaggc aaattccatt ttttcccttg 300
 t 301

<210> 287
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 287
 tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg 60
 cccagaagga acgtagagat cagatattac aacagctttg ttttgagggt tagaaatatg 120
 aaatgatttg gttatgaacg cacagtttag gcagcagggc cagaatcctg accctctgcc 180
 ccgtggttat ctctctccca gcttggctgc ctcatgttat cacagtattc cattttgitt 240
 gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggtaatgc 300
 t 301

<210> 288
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 288
 gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60
 agtcaatagg aagacaaatt ccagttccag ctcatctggg gtatctgcaa agctgcaaaa 120
 gatcttttaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatat 180
 aaaagcatct gcttttTgtga ttttaatttag ctcatctggc cactggaaga atccaaacag 240
 tctgccttaa ttttggatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300
 a 301

<210> 289
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (301)
 <223> n = A,T,C or G

<400> 289

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ggtagactgt ttccatgtta tgtttctata cattgctacc tcagtgtcc tggaaactta      60
gcttttgatg tctccaagta gtccaccttc atttaactct ttgaaactgt atcatctttg      120
ccaagtaaga gtggtggcct atttcagctg ctttgacaaa atgactgggt cctgacttaa      180
cgttctataa atgaatgtgc tgaagcaaag tgcccatggt ggcggcgaan aagagaaaga      240
tgtgttttgt tttggactct ctgtggtccc ttccaatgct gtgggtttcc aaccagnnga      300
a                                                                 301

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<210> 290

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 290

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acactgagct cttcttgata aatatacaga atgcttggca tatacaagat tctatactac      60
tgactgatct gttcatttct ctcacagctc ttacccccc aaagcttttcc accctaagtg      120
ttctgacctc cttttctaata cacagtaggg atagaggcag anccacctac aatgaacatg      180
gagttctatc aagaggcaga aacagcacag aatcccagtt ttaccattcg ctacgagtgc      240
tgcccttgaa aaaaacattt ctccatgtct cattttcttc atgcctcaag taacagtgag      300
a                                                                 301

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<210> 291

<211> 301

<212> DNA

<213> Homo sapien

<400> 291

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caggtaacca tttcttctat cctagaaaca tttcatttta tgttggtgaa acataacaac      60
tatatcagct agattttttt tctatgctt acctgctatg gaaaatttga cacattctgc      120
tttactcttt tgtttatagg tgaatcacaa aatgtatttt tatgtattct gtagttcaat      180
agccatggct gtttacttca ttttaatttat ttagcataaa gacattatga aaaggcctaa      240
acatgagctt cacttcccca ctaactaatt agcatctggt atttcttaac cgtaaatgct      300
a                                                                 301

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<210> 292

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 292

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accttttagt agtaatgtct aataataaat aagaaatcaa ttttataagg tccatatagc      60
tgtattaaat aatttttaag tttaaaagat aaaataocat cattttaaat gttggtattc      120
aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaatgat ttgcnagatg      180
ggaaatatag tasttyatga atgttnatta aattocagtt ataatagtgg ctacacactc      240
tcactacaca cacagacccc acagtcctat atgocacaaa cacatttcca taacttgaaa      300
a                                                                 301

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<210> 293
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 293
 ggtaccaagt gctggtgccg gcctgttacc tgtttctact gaaaagtctg gctaagtctc 60
 ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggccctagagc actgactgtt 120
 aacacaaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaaa gctgttctgt 180
 gtgagaattt tttaaaaggc tacttgtata ataacccttg tcatttttaa tgtacctcgg 240
 ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gctcgagcat 300
 g 301

<210> 294
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (301)
 <223> n = A,T,C or G

<400> 294
 tgacccataa caatatacac tagctatctt tttaaactgtc catcattagc accaatgaag 60
 attcaataaa attaccttta ttcacacatc tcaaaacaat tctgcaaatt cttagtgaag 120
 tttaaactata gtcacaganc ttaaataatc acattgtttt ctatgtctac tgaaaataag 180
 ttctactatt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc 240
 cccaattata cagtagcaca accaccttat gtagtcttta catgatagct ctgtagaggt 300
 t 301

<210> 295
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 295
 gtactctttc tctccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta 60
 cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac 120
 ttggtttgtg aatccatctt gcttttccc cattggaact agtcattaac ccattctctga 180
 actggtagaa aaacrctctga agagctagtc tatcagcatc tgacagggtga attggatggg 240
 tctcagaacc atttcacca gacagcctgt ttctatcctg tttataaat tagtttgggt 300
 tctct 305

<210> 296
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 296
 aggtactatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct 60
 cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg 120
 attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac 180
 ttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt 240

tgtcattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg 300
c 301

<210> 297

<211> 300

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(300)

<223> n = A,T,C or G

<400> 297

actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta 60
aagggttttga aaaccttgaa ggagaatcat ttgacaaga agtacttaag agtctagaga 120
acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt 180
tccatcattg ggagtgcact ggocatccct caaaatttgt ctgggctggc ctgagtggc 240
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc acactggcgg 300

<210> 298

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 298

tatgggggttt gtcacocaaa agctgatgct gagaaaggcc tccctggggc cccctcccgcg 60
ggcatctgag agacctggtg ttccagtgtt tctggaaatg ggtcccagtg ccgcccggctg 120
tgaagctctc agatcaatca cgggaagggc ctggcggtgg tggccacctg gaaccacctt 180
gtcctgtctg ttacatttc actaycagg tttctctggg cattacnatt tgttccccta 240
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcagggtggc ctcagcgagg 300
t 301

<210> 299

<211> 301

<212> DNA

<213> Homo sapien

<400> 299

gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca gggctctotgc 60
tcaactgcacc ctctgectcc caggttcagag caattctcct gctcagcct cccaggtagc 120
tgggattgca ggctcacgcc accataocca gctaattttt ttgtattttt agtagagacg 180
gagtttcgcc atgttggeca gctggctcct aactcctgac ctcaagcgac ctgectgcct 240
cggcctccca aagtgctgga attataggca tgagtcaaca cggccagcct aaagatatct 300
t 301

<210> 300

<211> 301

<212> DNA

<213> Homo sapien

<400> 300

attcagtttt	atttgctgcc	ccagtatctg	taaccaggag	tgccacaaaa	tcttgccaga	60
tatgtccac	accactggg	aaaggctccc	acctggctac	ttcctctatc	agctgggtca	120
gctgcattcc	acaaggttct	cagcctaata	agtttcta	cctgccagtc	tcaaaactta	180
gtaaagcaag	accatgacat	tccccacgg	aaatcagagt	ttgccccacc	gtcttggtac	240
tataaagcct	gcctctaaca	gtccttgctt	cttcacacca	atccccgagc	catcccccat	300
g						301

<210> 301

<211> 301

<212> DNA

<213> Homo sapien

<400> 301

ttaaattttt	gagaggataa	aaaggacaaa	taatctagaa	atgtgtcttc	ttcagtctgc	60
agaggacccc	aggtctccaa	gcaaccacat	ggtcaagggc	atgaataatt	aaaagtgggt	120
gggaactcac	aaagaccctc	agagctgaga	caccacaac	agtgggagct	cacaaagacc	180
ctcagagctg	agacaccac	aacagtggga	gctcacaag	accctcagag	ctgagacacc	240
cacaacagca	cctcgttcag	ctgccacatg	tgtgaataag	gatgcaatgt	ccagaagtgt	300
t						301

<210> 302

<211> 301

<212> DNA

<213> Homo sapien

<400> 302

aggtacacat	ttagcttggt	gtaaatgact	cacaaaactg	attttaaaat	caagttaatg	60
tgaattttga	aaattactac	ttaatcctaa	ttcacaataa	caatggcatt	aaggtttgac	120
ttgagttggt	tcttagtatt	atztatggta	aataggctct	taccacttgc	aaataactgg	180
ccacatcatt	aatgactgac	ttcccagtaa	ggctctctaa	ggggtaagta	ggaggatcca	240
caggatttga	gatgctaagg	ccccagagat	cgtttgatcc	aaccctctta	ttttcagagg	300
g						301

<210> 303

<211> 301

<212> DNA

<213> Homo sapien

<400> 303

aggtaccaac	tgtggaaata	ggtagaggat	cattttttct	ttccatatca	actaagttgt	60
atattgtttt	ttgacagttt	aacacatctt	cttctgtcag	agattctttc	acaatagcac	120
tggctaattg	aactaccgct	tgcattgtaa	aaatgggtgt	ttgtgaaatg	atcataggcc	180
agtaacgggt	atgtttttct	aactgatctt	ttgctcgttc	caaagggacc	tcaagacttc	240
catcgatttt	atatctgggg	tctagaaaag	gagttaatct	gttttccctc	ataaattcac	300
c						301

<210> 304

<211> 301

<212> DNA

<213> Homo sapien

<400> 304

acatggatgt	tattttgcag	actgtcaacc	tgaatttga	tttgcttgac	attgccta	60
------------	------------	------------	-----------	------------	----------	----

tattagtttc	agtttcagct	taccactttt	ttgtctgcaa	catgcaraas	agacagtgcc	120
cttttttagtg	tatcatatca	ggaatcatct	cacattgggt	tgtgccatta	ctgggtgcagt	180
gactttcagc	cacttgggta	aggtggagtt	ggccatatgt	ctccactgca	aaattactga	240
ttttcctttt	gtaattaata	agtgtgtgtg	tgaagattct	ttgagatgag	gtatataatct	300
c						301

<210> 305

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 305

gangtacagc	gtgggtcaagg	taacaagaag	aaaaaaaaatgt	gagtggcatc	ctgggatgag	60
caggggggaca	gacctggaca	gacacgttgt	catttgctgc	tgtgggtagg	aaaatgggag	120
taaaggaggga	gaaacagata	caaaatctcc	aactcagtat	taagggtattc	tcattgcctag	180
aatattggta	gaaacaagaa	tacattcata	tggcaataaa	ctaaccatgg	tggaaacaaaa	240
ttctgggatt	taagttggat	accaangaaa	ttgtattaaa	agagctgttc	atggaataag	300
a						301

<210> 306

<211> 8

<212> PRT

<213> Homo sapien

<400> 306

Val	Leu	Gly	Trp	Val	Ala	Glu	Leu
1				5			

<210> 307

<211> 637

<212> DNA

<213> Homo sapien

<400> 307

acaggggratg	aaggggaaagg	gagaggatga	ggaagcccc	ctggggattt	ggtttgggtcc	60
ttgtgatcag	gtgggtctatg	gggttatcc	ctacaaagaa	gaatccagaa	ataggggcac	120
attgaggaat	gatacttgag	cccaaagagc	attcaatcat	tgttttattt	gccttmtttt	180
cacaccattg	gtgaggagg	gattaocacc	ctgggggttat	gaagatgggt	gaacacccca	240
cacatagcac	cggagatatg	agatcaacag	tttcttagcc	atagagattc	acagcccaga	300
gcaggaggac	gcttgcacac	catgcaggat	gacatggggg	atgcgctcgg	gattgggtgtg	360
aagaagcaag	gactgttaga	ggcaggcttt	atagtaacaa	gacgggtggg	caaactctga	420
tttccgtggg	ggaatgtcat	ggtcttgctt	tactaagttt	tgagactggc	aggtagtga	480
actcattagg	ctgagaacct	tgtggaatgc	acttgaccca	scgatagag	gaagtagoca	540
ggtgggagcc	tttccagtg	ggtgtgggac	atatctggca	agattttgtg	gcactcctgg	600
ttacagatac	tggggcagca	aataaaactg	aatcttg			637

<210> 308

<211> 647

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(647)

<223> n = A,T,C or G

<400> 308

acgattttca	ttatcatgta	aatcgggtca	ctcaaggggc	caaccacagc	tgggagccac	60
tgctcagggg	aaggttcata	tgggactttc	tactgcccaa	ggttctatac	aggatataaa	120
ggngcctcac	agtatagatc	tggtagcaaa	gaagaagaaa	caaacactga	tctctttctg	180
ccaccctctc	gaccctttgg	aactcctctg	accctttaga	acaagcctac	ctaatatctg	240
ctagagaaaa	gaccaacaac	ggcctcaaa	gatctcttac	catgaaggct	tcagctaatt	300
cttggctaag	atgtgggttc	cacattaggt	tctgaatatg	gggggaaggg	tcaatttgct	360
catttttgtg	gtggataaag	tcaggatgcc	cagggggccag	agcagggggc	tgcttgcttt	420
gggaacaatg	gctgagcata	taaccatagg	ttatggggaa	caaaacaaca	tcaaagtcac	480
tgtatcaatt	gccatgaaga	cttgagggg	ctgaatctac	cgattcatct	taaggcagca	540
ggaccagttt	gagtggcaac	aatgcagcag	cagaatcaat	ggaaacaaca	gaatgattgc	600
aatgtccttt	tttttctcct	gcttctgact	tgataaaaagg	ggaccgt		647

<210> 309

<211> 460

<212> DNA

<213> Homo sapien

<400> 309

actttatagt	ttaggctgga	cattggaaaa	aaaaaaaaagc	cagaacaaca	tgtgatagat	60
aatatgattg	gctgcacact	tccagactga	tgaatgatga	acgtgatgga	ctattgtatg	120
gagcacatct	tcagcaagag	ggggaaatac	tcattcatttt	tggccagcag	ttgtttgatc	180
accaaacatc	atgccagaat	actcagcaaa	ccttcttagc	tcttgagaag	tcaaagtccg	240
ggggaattta	ttcctggcaa	ttttaattgg	actccttatg	tgagagcagc	ggctaccacg	300
ctggggtggt	ggagcgaaac	cgtcactagt	ggacatgcag	tggcagagct	cctggtaacc	360
acctagagga	atacacaggc	acatgtgtga	tgccaagcgt	gacacctgta	gcactcaaat	420
ttgtcttgtt	tttgtctttc	ggtgtgtaag	attcttaagt			460

<210> 310

<211> 539

<212> DNA

<213> Homo sapien

<400> 310-

acgggactta	tcaaataaag	ataggaaaag	aagaaaactc	aaatattata	ggcagaaatg	60
ctaaagggtt	taaaatatgt	caggattgga	agaaggcatg	gataaagaac	aaagttcagt	120
taggaaagag	aaacacagaa	ggaagagaca	caataaaaagt	cattatgtat	tctgtgagaa	180
gtcagacagt	aagattttgt	ggaaatgggt	tggtttgttg	tatggtatgt	attttagcaa	240
taatctttat	ggcagagaaa	gctaaaatcc	tttagcttgc	gtgaatgatc	acttgctgaa	300
ttcctcaagg	taggcatgat	gaaggagggt	ttagaggaga	cacagacaca	atgaactgac	360
ctagatagaa	agccttagta	tactcagcta	ggaatagtga	ttctgagggc	acactgtgac	420
atgattatgt	cattacatgt	atggtagtga	tggggatgat	aggaaggaag	aacttatggc	480
atattttcac	ccccacaaaa	gtcagttaaa	tattgggaca	ctaaccatcc	aggtcaaga	539

<210> 311

<211> 526

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (526)

<223> n = A,T,C or G

<400> 311

caaatttgag ccaatgacat agaattttac aaatcaagaa gcttattctg gggccatttc	60
ttttgacgtt tttctctaaac tactaaagag gcattaatga tccataaatt atattatcta	120
catttacagc atttaaaatg tgttcagcat gaaatattag ctacagggga agctaaataa	180
attaacatg gaataaagat ttgtccttaa atataatcta caagaagact ttgatatttg	240
tttttcacaa gtgaagcatt cttataaagt gtcataacct ttttggggaa actatgggaa	300
aaaatgggga aactctgaag ggttttaagt atcttacctg aagctacaga ctccataacc	360
tctctttaca gggagctcct gcagccocta cagaaatgag tggctgagat tcttgattgc	420
acagcaagag cttctcatct aaaccctttc ctttttagt atctgtgtat caagtataaa	480
agttctataa actgtagtnt acttatttta atcccaaag catagt	526

<210> 312

<211> 500

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (500)

<223> n = A,T,C or G

<400> 312

cctctctctc cccacccoct gactctagag aactggggtt tctccagta ctccagcaat	60
tcattttctga aagcagttga gacactttat tccaaagtac actgcagatg ttcaaactct	120
ccattttctt tcccttcca cctgocagtt ttgttgactc tcaacttgtc atgagtgtaa	180
gcattaagga cattatgctt cttcgattct gaagacaggc cctgctcatg gatgactctg	240
gcttcttagg aaaatatttt tcttccaaaa tcagtaggaa atctaaactt atccctctt	300
tgcagatgtc tagcagcttc agacatttgg ttaagaacct atgggaaaaa aaaaaactct	360
tgctaattgt gtttcccttg taaaccanga ttcttatttg nctggatatag aatatcagct	420
ctgaacgtgt ggtaaagatt tttgtgttg aatataggag aaatcagttt gctgaaaagt	480
tagtcttaat tatctattgg	500

<210> 313

<211> 718

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (718)

<223> n = A,T,C or G

<400> 313

ggagatttgt gtggtttgca gccgagggag aecaggaaga tctgcatggt gggaaggacc	60
tgatgataca gaggtgagaa ataagaaagg ctgetgactt taccatctga ggccacacat	120
ctgctgaaat ggagataatt aacatcacta gaaacagcaa gatgacaata taatgtctaa	180
gtagtacat gtttttgcac atttccagcc ctttttaaata tccacacaca caggaagcac	240
aaaaggaagc acagagatcc ctgggagaaa tgcccggccg ccatcttggg tcatcgatga	300
gcctgcctt gtgcctgntc ccgcttctga gggaaggaca ttagaaaaatg aattgatgtg	360
ttccttaaaag gatggcagga aaacagatcc tgtctgtgat atttatttga acgggattac	420

agatttgaaa	tgaagtcaca	aagtgagcat	taccaatgag	aggaaaacag	acgagaaaat	480
cttgatgggt	cacaagacat	gcaacaaaca	aaatggaata	ctgtgatgac	acgagcagcc	540
aactggggag	gagataccac	ggggcagagg	tcaggattct	ggccctgctg	cctaactgtg	600
cgttatacca	atcatttcta	tttctaccct	caaacaagct	gtngaatatc	tgacttacgg	660
ttcttntggc	ccacattttc	atnateccacc	ccntcncnttt	aannttantc	caaantgt	718

<210> 314

<211> 358

<212> DNA

<213> Homo sapien

<400> 314

gtttattttac	attacagaaa	aaacatcaag	acaatgtata	ctattttcaa	tatatccata	60
cataatcaaa	tatagctgta	gtacatgttt	tcattgggtg	agattaccac	aaatgcaagg	120
caacatgtgt	agatctcttg	tcttattctt	ttgtctataa	tactgtattg	tgtagtccaa	180
gctctcggtg	gtccagccac	tgtgaaacat	gtcccttta	gattaacctc	gtggacgctc	240
ttgttgtatt	gctgaactgt	agtgccctgt	attttgcttc	tgtctgtgaa	ttctgttgct	300
tctggggcat	ttccttgtga	tgcagaggac	caccacacag	atgacagcaa	tctgaatt	358

<210> 315

<211> 341

<212> DNA

<213> Homo sapien

<400> 315

taccacctcc	ccgctggcac	tgatgagccg	catcaccatg	gtcaccagca	ccatgaaggc	60
ataggatgat	atgaggacat	ggaatgggcc	cccaaggatg	gtctgtccaa	agaagcgagt	120
gacccccatt	ctgaagatgt	ctggaacctc	taccagcagg	atgatgatag	ccccaatgac	180
agtcaccagc	tccccgacca	gccggatata	gtccttaggg	gtcatgtagg	cttcttgaag	240
tagcttctgc	tgtgaagagg	tgttgtcccc	ggggctcgtg	cggttattgg	tcctgggctt	300
gagggggcgg	tagatgcagc	acatggtgaa	gcagatgatg	t		341

<210> 316

<211> 151

<212> DNA

<213> Homo sapien

<400> 316

agactgggca	agactcttac	gccccacact	gcaatttggt	cttggtgccg	tatccattta	60
tgtgggcctt	tctcgagttt	ctgattataa	acaccactgg	agcgatgtgt	tgactggact	120
cattcagggg	gctctgggtg	caatattagt	t			151

<210> 317

<211> 151

<212> DNA

<213> Homo sapien

<400> 317

agaactagtg	gacccctaatg	aaataacctga	aacatatatt	ggcatttata	aatgggctcaa	60
atcttcattt	atctctggcc	taaaccctgg	ctcctgaggc	tgccggccagc	agatcccagg	120
ccagggctct	gttcttgcca	cacctgcttg	a			151

<210> 318

<211> 151

<212> DNA

<213> Homo sapien

<400> 318

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actggtggga ggcgctgttt agttggctgt tttcagaggg gtctttcggg gggacctcct      60
gctgcaggct ggagtgtctt tattcctggc gggagaecgc acattccact gctgaggctg      120
tgggggcggt ttatcaggca gtgataaaca t                                     151
```

<210> 319

<211> 151

<212> DNA

<213> Homo sapien

<400> 319

```
aactagtggg tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta      60
catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg      120
taagattggg tttatgtgat ttttagtggg a                                     151
```

<210> 320

<211> 150

<212> DNA

<213> Homo sapien

<400> 320

```
aactagtggg tccactagtc cagtgtgggtg gaattccatt gtgttggggg tctagatcgc      60
gagcggtcgc cttttttttt tttttttttg ggggggaatt tttttttttt aatagttatt      120
gagtgttcta cagcttacag taaataccat                                     150
```

<210> 321

<211> 151

<212> DNA

<213> Homo sapien

<400> 321

```
agcaactttg tttttcatcc aggttatitt aggcttagga tttcctctca cactgcagtt      60
taggggtggc ttgtaaecag ctatggcata ggtgttaacc aaaggctgag taaacatggg      120
tgcctctgag aaatcaaagt cttcatacac t                                     151
```

<210> 322

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (151)

<223> n = A,T,C or G

<400> 322

```
atccagcatc ttctctgtt tcttgecttc ctttttcttc ttcttasatt ctgcttgagg      60
tttgggcttg gtcagtttgc cacagggctt ggagatgggt acagtcttct ggcattcggc      120
attgtgcagg gctcgcttca naattccagt t                                     151
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<210> 323

<211> 151

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 323

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nagactcant tactacccag tttgtgggtt twtggggagaa atgtaactgg acagtttagct	120
gttcaatyaa aaagacactt ancccatgtg g	151

<210> 324

<211> 461

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(461)

<223> n = A,T,C or G

<400> 324

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agaagtggc agctaaagga atccagggtt tggttggtac ttttaataacc tttgatgaaa	120
agagttacta cgaatcccat cttgggtcca gctatatcac tgacagcatg gtagaagact	180
gcgaacctca cttctagact ttccaggtgg gacgaaacgg gttcagaaac tgcagggggc	240
ctcatacagg gatatacaaaa taccctttgt gtaacccagg ccctggggaa tcagggtgact	300
cacacaaatg caatagttgg tcaactgcatt tttacctgaa ccaaagctaa acccggtgtt	360
gccaccatgc accatggcat gccagagttc aacactgttg ctcttgaaaa ttgggtctga	420
aaaaacgcac aagagcccct gccctgcctt agctgangca c	461

<210> 325

<211> 400

<212> DNA

<213> Homo sapien

<400> 325

acactgtttc catgttatgt ttctacacat tgctacctca gtgtccttgg aaacttagct	60
tttgatgtct ccaagtagtc caccttcatt taactctttg aaactgtatc atctttgcc	120
agtaagagtg gtggcctatt tcagctgctt tgacaaaatg actggctcct gacttaacgt	180
tctataaatg aatgtgctga agcaaagtgc ccatgggtggc ggcgaagaag agaaagatgt	240
gttttgtttt ggaactctctg tggctccttc caatgctgtg ggtttccaac caggggaagg	300
gtcccttttg cattgccaag tgccataacc atgagcacta cgctaccatg gttctgcctc	360
ctggccaagc aggtggttt gcaagaatga aatgaatgat	400

<210> 326

<211> 1215

<212> DNA

<213> Homo sapien

<400> 326

ggaggactgc agcccgcact cgcagccctg gcaggcggca ctggctcatgg aaaacgaatt	60
gttctgctcg ggcgtcctgg tgcacccgca gtgggtgctg tcagccgcac actgtttcca	120
gaactcctac accatcgggc tgggcctgca cagtcttgag gccgaccaag agccagggag	180

ccagatggtg	gaggccagcc	tctccgtacg	gcaccagag	tacaacagac	ccttgctcgc	240
taacgacctc	atgctcatca	agttggacga	atccgtgtcc	gagtctgaca	ccatccggag	300
catcagcatt	gcttcgcagt	gocctaccgc	ggggaactct	tgccctcggtt	ctggctgggg	360
tctgctggcg	aacggcagaa	tgccctaccgt	gctgcagtgc	gtgaacgtgt	cgggtggtgtc	420
tgaggaggtc	tgacagtaagc	tctatgaccc	gctgtaccac	cccagcatgt	tctgcgccgg	480
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acagtgcocc	cttggtggac	gttgacccaa	ccttaccagt	tggtttttca	ttttttgtcc	1140
ctttccccta	gtccagaaa	taaagtctaa	gagaagcgca	aaaaaaaaaa	aaaaaaaaaa	1200
aaaaaaaaaa	aaaaa					1215

<210> 327

<211> 220

<212> PRT

<213> Homo sapien

<400> 327

Glu	Asp	Cys	Ser	Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Val	Met
1			5					10						15	
Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val
	20						25						30		
Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu	Gly
	35						40					45			
Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val	Glu
	50					55				60					
Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu	Ala
65				70					75					80	
Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser	Asp
		85					90							95	
Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly	Asn
	100						105						110		
Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg	Met	Pro
	115				120							125			
Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu	Glu	Val	Cys
	130				135						140				
Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe	Cys	Ala	Gly
145				150					155					160	
Gly	Gly	Gln	Asp	Gln	Lys	Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly	Gly	Pro
		165				170							175		
Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly	Lys	Ala
	180					185							190		
Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu	Cys	Lys
	195					200						205			
Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser				
	210					215					220				

<210> 328

<211> 234

<212> DNA

<213> Homo sapien

<400> 328

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agccctggca ggcggcactg gtcattggaaa acgaattgtt ctgctcgggc gtcctgggtgc      120
atccgcagtg ggtgctgtca gccacacact gtttccagaa ctctacacc atcggggtgg      180
gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag gcca      234

```

<210> 329

<211> 77

<212> PRT

<213> Homo sapien

<400> 329

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Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly Glu Asp Cys Ser
 1              5              10              15
Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu
      20              25              30
Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Thr
      35              40              45
His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu
      50              55              60
Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala
65              70              75

```

<210> 330

<211> 70

<212> DNA

<213> Homo sapien

<400> 330

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cccaacacaa tggcccgatc ccattccctga ctccgccctc aggatcgctc gtctctggta      60
gctgcagcca                                     70

```

<210> 331

<211> 22

<212> PRT

<213> Homo sapien

<400> 331

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Gln His Asn Gly Pro Ile Pro Ser Leu Thr Pro Pro Ser Gly Ser Leu
 1              5              10              15
Val Ser Gly Ser Cys Ser
      20

```

<210> 332

<211> 2507

<212> DNA

<213> Homo sapien

<400> 332

```

tgggtgccgct gcagccggca gagatgggtg agctcatggt cccgctggtg ctctctcttc      60
tgcccttctt tctgtatatg gctgcgcccc aaatcaggaa aatgctgtcc agtgggggtg      120

```


gtacatcaac	tgttcagctt	cctgggaaag	tagttgtggt	cacaggagct	aatacaggta	180
tcgggaagga	gacagccaaa	gagctggctc	agagaggagc	tcgagtatat	ttagcttgcc	240
gggatgtgga	aaagggggaa	ttggtggcca	aagagatcca	gaccacgaca	gggaaccagc	300
aggtgttggt	gcggaaactg	gaactgtctg	atactaagtc	tattcgagct	tttgctaagg	360
gcttcttagc	tgaggaaaag	cacctocacg	ttttgatcaa	caatgcagga	gtgatgatgt	420
gtccgtactc	gaagacagca	gatggctttg	agatgcacat	aggagtcaac	cacttgggtc	480
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agggcaagca	cccaggactg	atgagggtctt	aacaaaaacc	agtgtggcaa	aaaaaaaaaa	1920
aaaaaaaaaa	aaaaatccta	aaaacaaaca	aacaaaaaaa	acaattcttc	attcagaaaa	1980
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cttacattgt	cttgacaaga	ttaaaatgtc	tgtgocaaaa	ttttgtattt	tatttgagga	2100
cttcttatca	aaagtaatgc	tgocaaagga	agtctaagga	attagtagtg	ttcccatcac	2160
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cttttatatg	acctgttttg	accattaagc	tatatgttta	gaaatgggtca	ttttacggaa	2340
aaattagaaa	aattctgata	atagtgcaga	ataaatgaat	taatgtttta	cttaatttat	2400
attgaactgt	caatgacaaa	taaaaattct	ttttgattat	tttttgtttt	catttaocag	2460
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<210> 333

<211> 3030

<212> DNA

<213> Homo sapien

<400> 333

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ggagagcgag	ctgggtgccc	cctagattcc	ccgccccgc	acctcatgag	ccgacctcg	120
gctccatgga	gcccggcaat	tatgcccact	tggatggagc	caaggatata	gaaggcctgc	180
tgggagcggg	agggggggcg	aatctggctg	cccactcocc	tctgaccagc	caaccagogg	240
cgctacgct	gatgcotgct	gtcaactatg	ccccccttga	tctgccaggc	tcggcgaggc	300
cgccaaagca	atgccaccca	tgccctgggg	tgcccagggg	gacgtcccca	gctcccgtgc	360
cttatggtta	ctttggaggc	gggtactact	cctgcggagt	gtccgggagc	tcgctgaaac	420
cctgtgccc	ggcagccacc	ctggccgcgt	accccgcgga	gactcccacg	gcccgggaag	480

agtaccccag	ycgccccact	gagtttgcc	tctatccggg	atatccggga	acctaccagc	540
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acagccagat	gtgttgccag	ggagaacaga	acccaccagg	tcccttttg	aaggcagcat	720
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<210> 334

<211> 2417

<212> DNA

<213> Homo sapien

<400> 334

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agttttacaaa	tgaggaaaca	ggtgcaaaaa	ggttggtacc	tgtcaaaggt	cgtatgtggc	180
agagccaaga	tttgagccca	gttatgtctg	atgaacttag	cctatgctct	ttaaacttct	240
gaatgctgac	cattgaggat	atctaaactt	agatcaattg	cattttccct	ccaagactat	300

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<210> 335

<211> 2984

<212> DNA

<213> Homo sapien

<400> 335

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<210> 336

<211> 147

<212> PRT

<213> Homo sapien

<400> 336

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20	25	30			
Pro Lys Gln	Pro Gln Lys	Arg Ser Arg	Ala Ala Phe	Ser His Thr	Gln
35	40	45			
Val Ile Glu	Leu Glu Arg	Lys Phe Ser	His Gln Lys	Tyr Leu Ser	Ala
50	55	60			
Pro Glu Arg	Ala His Leu	Ala Lys Asn	Leu Lys Leu	Thr Glu Thr	Gln
65	70	75		80	

115

Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
 85 90 95
 Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala
 100 105 110
 Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn
 115 120 125
 Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro
 130 135 140
 Ala Phe Trp
 145

<210> 337
 <211> 9
 <212> PRT
 <213> Homo sapien

<400> 337
 Ala Leu Thr Gly Phe Thr Phe Ser Ala
 1 5

<210> 338
 <211> 9
 <212> PRT
 <213> Homo sapien

<400> 338
 Leu Leu Ala Asn Asp Leu Met Leu Ile
 1 5

<210> 339
 <211> 318
 <212> PRT
 <213> Homo sapien

<400> 339
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 20 25 30
 Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
 50 55 60
 Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
 65 70 75 80
 Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
 85 90 95
 Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
 100 105 110
 Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
 115 120 125
 Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met
 130 135 140
 His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu

145 150 155 160
 Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser
 165 170 175
 Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly
 180 185 190
 Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala
 195 200 205
 Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly
 210 215 220
 Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val
 225 230 235 240
 Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe
 245 250 255
 Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu
 260 265 270
 Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His
 275 280 285
 Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg
 290 295 300
 Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp
 305 310 315

<210> 340
 <211> 483
 <212> DNA
 <213> Homo sapien

<400> 340
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 ctctgctgc aggtggagt gtctttattc ctggcgggag accgcacatt cactgctga 180
 gggtgtgggg gcggtttatc aggcagtgat aaacataaga tgctatttcc ttgactccgg 240
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 gctccaaacg tgacatcact gatgctcttc tcgggggtgc tgatggcccg cttgggtcacg 360
 tgctcaatct cgccattcga ctcttgctcc aaactgtatg aagacacctg actgcacgtt 420
 tttctgggc ttccagaatt taaagtgaag ggcagcactc ctaagctccg actccgatgc 480
 ctg 483

<210> 341
 <211> 344
 <212> DNA
 <213> Homo sapien

<400> 341
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 gctgccttac aagtattaaa tattttactt ctttccataa agagtagctc aaaatatgca 180
 attaatataa taatttctga tgatgggttt atctgcagta atatgtatat catctattag 240
 aatttactta atgaaaaact gaagagaaca aaatttgtaa ccactagcac ttaagtactc 300
 ctgattctta acattgtctt taatgaccac aagacaacca acag 344

<210> 342
 <211> 592
 <212> DNA
 <213> Homo sapien

<400> 342

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cctggcaggt	aaaccaatgc	caagagagtg	atggaaaacca	ttggcaagac	tttgttgatg	180
accaggattg	gaattttata	aaaatattgt	tgatgggaag	ttgctaaagg	gtgaattact	240
tccttcagaa	gagtgtaaag	aaaagt-caga	gatgctataa	tagcagctat	tttaattggc	300
aagtgccact	gtggaaagag	ttcctgtgtg	tgctgaagtt	ctgaagggca	gtcaaattca	360
tcagcatggg	ctgtttgggtg	caaatgcaaa	agcacaggtc	tttttagcat	gctggctctc	420
cccgtgtcct	tatgcaaaata	atcgtcttct	tctaaatttc	tcctaggctt	cattttccaa	480
agttcttctt	ggtttgtgat	gtctttcttg	ctttccatta	attctataaa	atagtatggc	540
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<210> 343

<211> 382

<212> DNA

<213> Homo sapien

<400> 343

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ctgactgccc	aaggggctca	gaaccccagc	aatcccttcc	tttcaatacc	ttcttttttg	300
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aaaccaccaa	gctgaaaaaa	aa				382

<210> 344

<211> 536

<212> DNA

<213> Homo sapien

<400> 344

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ccttcttatt	atttgatcta	gaaattgccc	tctttttacc	cctaocatga	gccctacaaa	420
caactaacct	gccactaata	gttatgtcat	ccctcttatt	aatcatcatc	ctagccctaa	480
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<210> 345

<211> 251

<212> DNA

<213> Homo sapien

<400> 345

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gcgtggggca	ggaaatcaca	tactacactg	cccaggagcc	agacacattt	atggaacaga	180
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gtgccatttc	c					251

<210> 346
 <211> 282
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(282)
 <223> n = A,T,C or G

<400> 346
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 agggagacta tacctgggtc ttgccctaag tgagaggtct tccctcccg accaaaaaat 180
 agaaaggctt tctatttcac tggcccaggt agggggaagg agagtaactt tgagtctgtg 240
 ggtctcattt cccaaggtgc cttcaatgct catnaaaacc aa 282

<210> 347
 <211> 201
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(201)
 <223> n = A,T,C or G

<400> 347
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 tctgagactg actggaccca cccagaccca gggcaaagat acatgttacc atatcatctt 180
 tataaagaat ttttttttgt c 201

<210> 348
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 348
 ctgttaatca caacatttgt gcatcacttg tgccaagtga gaaaatgttc taaaatcaca 60
 agagagaaca gtgccagaat gaaactgacc ctaagtccca ggtgcccctg ggcaggcaga 120
 aggagacact cccagcatgg aggaggggtt atcttttcat cctaggtcag gtctacaatg 180
 ggggaagggtt ttattataga actcccaaca gccacacctc ctcctgccac ccacccgatg 240
 gccttgccctc c 251

<210> 349
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 349
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 aacccctgag gatgccagag ctatgggtcc agaacatggt gtgggtattat caacagagtt 120
 cagaaggggtc tgaactctac gtgttaccag agaacataat gcaattcatg cattccactt 180
 agcaattttg taaaatacca gaaacagacc ccaagagtct ttcaagatga ggaaaaattca 240

actcctgggt t

251

<210> 350

<211> 908

<212> DNA

<213> Homo sapien

<400> 350

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ccacatacct	tgctcggaac	attacaatgg	cttctgcatg	catgggaagt	gtgagcattc	780
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<210> 351

<211> 472

<212> DNA

<213> Homo sapien

<400> 351

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cattaacttg	attttaaaat	cagwtttgyg	agtcatttac	cacaagctaa	atgtgtacac	180
tatgataaaa	acaaccattg	tattcctgtt	tttctaaaca	gtcctaattt	ctaactagt	240
atatatcctt	cgatcatcaat	gaactttgtt	ttcttttact	ccagtaataa	agtaggcaca	300
gatctgtcca	caacaaactt	gccctctcat	gccttgccct	tcacatgct	ctgctccagg	360
tcagccccct	tttggcctgt	ttgttttgtc	aaaaaoccaa	tctgcttctt	gcttttcttg	420
gtaatatata	tttaggggaag	atgttgcttt	gcccacacac	gaagcaaagt	aa	472

<210> 352

<211> 251

<212> DNA

<213> Homo sapien

<400> 352

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caggctgcgt	tcctgctcta	cgatgaagac	caagatgcag	tttccaaaca	ttgocactac	180
atacatggaa	aggaggggga	agccaaocca	gaaatgggct	ttctctaate	ctgggataacc	240
aataagcaca	a					251

<210> 353

<211> 436

<212> DNA

<213> Homo sapien

<400> 353

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gtatccaaaa	gcaaaacagc	agatatata	aattaaagag	acagaagata	gacattaaca	180
gataaggcaa	cttatacat	gacaatccaa	atccaataca	tttaaacatt	tgggaaatga	240
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tcattgtctga	raaggctctc	ccttcaatgg	ggatgacaaa	ctccaaatgc	cacacaaatg	360
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gggctcctaa	tgtagt					436

<210> 354

<211> 854

<212> DNA

<213> Homo sapien

<400> 354

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<210> 355

<211> 676

<212> DNA

<213> Homo sapien

<400> 355

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atccacaagt	catacctgga	tgtcagcgaa	gagggcacgg	aggcagcagc	agccactggg	180
gacagcatcg	ctgtaaaaag	cctaccaatg	agagctcagt	tcaaggcgaa	ccacccttct	240
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gtgactttcc	cacggccaaa	aagctgttca	cacctcacgc	acctctgtgc	ctcagtttgc	420
tcattctgcaa	aatagggtcta	ggatttcttc	caaccatttc	atgagttgtg	aagctaaggc	480
tttgtaatac	atggaaaaag	gtagacttat	gcagaaagcc	tttctggctt	ctttatctgt	540
ggtgtctcat	ttgagtgtcg	tccagtgcac	tgatcaagtc	aatgagtaaa	attttaaggg	600
attagatttt	cttgacttgt	atgtatctgt	gagatcttga	ataagtgacc	tgacatctct	660
gcttaaagaa	aaccag					676

<210> 356

<211> 574

<212> DNA

<213> Homo sapien

<400> 356

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caagcttccc	atttgttagat	ctcagtgcct	atgagtatct	gacacctgtt	cctctcttca	180
gtctcttagg	gaggcttaaa	tctgtctcag	gtgtgctaag	agtgcagcc	caaggkggtc	240
aaaagtccac	aaaactgcag	tctttgctgg	gatagtaagc	caagcagtgc	ctggacagca	300
gagttctttt	cttgggcaac	agataaccag	acaggactct	aatcgtgctc	ttattcaaca	360
ttcttctgtc	tctgcctaga	ctggaataaa	aagccaatct	ctctcgtggc	acaggaagg	420
agatacaagc	tcgtttacat	gtgatagatc	taacaaaggc	atctaccgaa	gtctgggtctg	480
gatagacggc	acagggagct	cttaggtcag	cgctgctggg	tggaggacat	tcttgagtcc	540
agctttgcag	cctttgtgca	acagtacttt	ccca			574

<210> 357

<211> 393

<212> DNA

<213> Homo sapien

<400> 357

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aagccacaac	caaracttga	ttttatcaac	aaaaaccctt	aatataaac	ggsaaaaaag	180
atagatataa	ttattccagt	ttttttaaaa	cttaaaarat	attccattgc	cgaattaara	240
araarataag	tggtatatgg	aaagaagggc	attcaagcac	actaaaraaa	cctgaggkaa	300
gcataatctg	tacaaaatta	aactgtcctt	tttggcattt	taacaaattt	gcaacgktct	360
tttttttctt	tttctgtttt	tttttttttt	tac			393

<210> 358

<211> 630

<212> DNA

<213> Homo sapien

<400> 358

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gcatagagta	gggaagctaa	tocagcacag	ggaggtcaca	gagacatccc	taaggaagtg	180
gagtttaaac	tgagagaagc	aagtgcctaa	actgaaggat	gtgttgaaga	agaagggaga	240
gtagaacaat	ttgggcagag	ggaaccttat	agacctaaag	gtgggaagggt	tcaaagaact	300
gaaagagagc	tagaacagct	ggagocgttc	tccgggtgtaa	agaggagtca	aagagataag	360
attaaagatg	tgaagattaa	gatcttgggtg	gcattcaggg	attggcactt	ctacaagaaa	420
tactgaagg	gagtaatgtg	acattacttt	tcacttcagg	atggccattc	taactocagg	480
gggtagactg	gactaggtaa	gactggaggc	aggtagaact	cttctaaggc	ctgcgatagt	540
gaaagacaaa	aataagtggg	gaaattcagg	ggatagttaa	aatcagtagg	acttaatgag	600
caagccagag	gttctctcac	aacaaccagt				630

<210> 359

<211> 620

<212> DNA

<213> Homo sapien

<400> 359

acagcattcc	aaaatatata	tctagagact	aarrgtaaat	gctctatagt	gaagaagtaa	60
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ctcaccagaa	gaataaagt	ctctgccagt	tattaaagga	ttactgctgg	tgaattaaat	180
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aggattaact	gttttaggaa	cagatataaa	gcttcgccac	ggaagagatg	gacaaagcac	300
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tgcaacatta	tgcttcatga	ataatatgta	gaaagaaggt	ctgatgaaaa	tgacatcctt	420
aatgtaagat	aactttataa	gaattctggg	tcaaataaaa	ttctttgaag	aaaacatcca	480
aatgtcattg	acttatcaaa	tactatcttg	gcatataacc	tatgaaggca	aaactaaaca	540
aacaaaaagc	tcacaccaaa	caaaaccatc	aacttatttt	gtattctata	acatacgaga	600
ctgtaaagat	gtgacagtgt					620

<210> 360

<211> 431

<212> DNA

<213> Homo sapien

<400> 360

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tactcatcat	ttttggccag	cagttgtttg	atcaccaaac	atcatgccag	aatactcagc	180
aaaccttctt	agctcttgag	aagtcaaagt	ccgggggaat	ttattcctgg	caattttaat	240
tggtactcctt	atgtgagagc	agcggctacc	cagctggggg	ggtggagcga	acccgtcact	300
agtggacatg	cagtggcaga	gctcctggta	accacctaga	ggaatacaca	ggcacatgtg	360
tgatgccaaag	cgtgacacct	gtagcactca	aatttgtctt	gtttttgtct	ttcgggtgtg	420
agattcttag	t					431

<210> 361

<211> 351

<212> DNA

<213> Homo sapien

<400> 361

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ttgggtctct	tggtctcttg	ccaagtttcc	cagccactcg	agggagaaat	atcgggaggt	180
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caatcctgga	ttcaatgtct	gaaacctcgc	tctctgcctg	ctggacttct	gaggccgtca	300
ctgccactct	gtcctccagc	tctgacagct	cctcatctgt	ggctctgttg	t	351

<210> 362

<211> 463

<212> DNA

<213> Homo sapien

<400> 362

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tgtagatgag	ccggctgaag	atcttgcgca	tgcgcggctt	cagggcgaaag	ttcttggcgc	120
ccccggtcac	agaaatgacc	aggttgggtg	ttttcagggtg	ccagtgtctgg	gtcagcagct	180
cgtaaaggat	ttccgcgtcc	gtgtcgcagg	acagacgtat	atacttccct	ttcttcccca	240
gtgtctcaaa	ctgaatatcc	ccaaaggcgt	cggtaggaaa	ttccttgggtg	tgtttcttgt	300
agttccattt	ctcacttttg	ttgatctggg	tgcttcccat	gtgctggctc	tgggcatagc	360
cacacttgca	cacattctcc	ctgataagca	cgatgggtgtg	gacaggaagg	aaggatttca	420
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<210> 363

<211> 653

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(653)

<223> n = A,T,C or G

<400> 363

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tgggaggcac tacgcaagat gggactgctg cctgggggtga gacatectct ccttgggagat      180
ctaacgaaac ttctcaccta tgagttgtaa agcagaaata cctgnactac agacgagtgc      240
ccaacagcaa cccccggaa gtatgagttc ctctrgggcc tccgttecta ocatgagasc      300
tagcaagatg naagtgttga gantcattgc agaggttcag aaaagagacc cntcgtgact      360
ggtctgcaca gttcatggag gctgcagatg aggccttggg tgctctggat gctgctgcag      420
ctgaggccga agccccgggt gaagcaagaa cccgcatggg aattggagat gaggctgtgt      480
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attttggaga tccntgggtcc agaattccat ttaccttctg ggccagatac caccagaatg      600
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<210> 364

<211> 401

<212> DNA

<213> Homo sapien

<400> 364

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aaaacaaggt ggaatgatct agaattgtaa cattttaaga aaacatagc atttgacaga      180
tgagaaagct caattataga tgcaaagtta taactaaact actatagtag taaagaaata      240
catttcacac ccttcatata aattcactat ctgggttga ggcactccat aaaatgtatc      300
acgtgcatag taaatcttta tatttgctat ggcgttgcac tagaggactt ggactgcaac      360
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<210> 365

<211> 356

<212> DNA

<213> Homo sapien

<400> 365

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atgtttcagt gctagagcgt aggaatagac cctggcgctc actgtgagat gttcttcagc      120
taccagagca tcaagtctct gcagcaggct attcttgggt aaagaaatga cttocacaaa      180
ctctccatcc cctggctttg gcttcggcct tgcgttttcg gcatcatctc cgtaaatggg      240
gactgtcacg atgtgtatag tacagtttga caagcctggg tocatacaga ccgctggaga      300
acattcggca atgtccctt tgtagccagt ttcttcttcg agtcccgga gagcag          356

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<210> 366

<211> 1851

<212> DNA

<213> Homo sapien

<400> 366

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tcattcaocat tgcacagcagc ggcaocgtta gtcaggtttt ctgggaatcc cacatgagta      60

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cttccgtggt	cttcattctt	cttcaatagc	cataaatctt	ctagctctgg	ctggctggtt	120
tcacttcctt	taagcctttg	tgactcttcc	tctgatgtca	gctttaagtc	ttggtctgga	180
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cctttgtcag	agctgtcctc	ttttgttgt	caaggacatt	aagttgacat	cgtctgtcca	720
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gctcctgaga	aacaccccag	ctcttccggt	ctaacacagg	caagtcaata	aatgtgataa	1620
tcacataaac	agaattaaaa	gcaaagtcac	ataagcatct	caacagacac	agaaaaggca	1680
tttgacaaaa	tccagcatcc	ttgtatttat	tgtygcagtt	ctcagaggaa	atgcttctaa	1740
cttttcccca	tttagtatta	tggtggctgt	gggcttgcca	taggtggttt	ttattacttt	1800
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<210> 367

<211> 668

<212> DNA

<213> Homo sapien

<400> 367

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ttcagtattt	tgaagataaa	atttgtatag	ctataccttg	ttttttgatt	cgatatcagc	120
accrtataag	agcagtgctt	tggccattaa	tttatctttc	attttagaca	gcrtagtgga	180
gagtggtatt	tccataactca	tctggaatat	ttggatcagt	gccatgttcc	agcaacatta	240
acgcacattc	atcttccctgg	cattgtacgg	cctgtcagta	ttagacccaa	aaacaaaatta	300
catatcttag	gaattcaaaa	taacattcca	cagctttcac	caactagtta	tatttaaagg	360
agaaaactca	tttttatgcc	atgtattgaa	atcaaaccga	cctcatgctg	atatagtgtg	420
ctactgcata	cctttatcag	agctgtcctc	ttttgttgt	caaggacatt	aagttgacat	480
cgtctgtcca	gcaggagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	540
gcagtcctat	gagagtgaga	agacttttta	ggaaattgta	gtgcactagc	tacagccata	600
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aaaaaaaa						668

<210> 368

<211> 1512

<212> DNA

<213> Homo sapien

<400> 368

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gaagtagtaa	aactcstgct	ggacagacga	tgtcaactta	atgtccttga	caacaaaaag	840
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gaacatggca	ctgatocaaa	tattccagat	gagtatggaa	ataccactct	rcactaygct	960
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gaaaacactg	aatttgtaaa	aggtaatact	tactattttt	caatttttcc	tctctaggat	1320
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<210> 369

<211> 1853

<212> DNA

<213> Homo sapien

<400> 369

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gccttcatgg	akcccaggta	ccacgtccrt	ggagaagatc	tggacaagct	ccacagagct	660
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caaaggctta	aaggaagtga	aaacagccag	ccagaggcat	ggaaactttt	aaatttaaac	1440
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gcggtgtctc	acgcctgtaa	ttccagcacc	ttgagaggct	gaggtgggca	gatcacgaga	1620
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<210> 370

<211> 2184

<212> DNA

<213> Homo sapien

<400> 370

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<210> 371
 <211> 1855
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1855)
 <223> n = A,T,C or G

<400> 371

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<210> 372
 <211> 1059
 <212> DNA
 <213> Homo sapien

<400> 372

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<210> 373

<211> 1155

<212> DNA

<213> Homo sapien

<400> 373

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<210> 374

<211> 2000

<212> DNA

<213> Homo sapien

<400> 374

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<210> 375

<211> 2040

<212> DNA

<213> Homo sapien

<400> 375

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<210> 376
 <211> 329
 <212> PRT
 <213> Homo sapien

<400> 376

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Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
35     40     45
Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
50     55     60
Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
65     70     75     80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
85     90     95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
100    105    110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
115    120    125
Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
130    135    140
Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
145    150    155    160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
165    170    175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
180    185    190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
195    200    205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
210    215    220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
225    230    235    240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
245    250    255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
260    265    270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
275    280    285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu

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290 295 300
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 305 310 315 320
 Ser Met Leu Phe Leu Val Ile Ile Met
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<210> 377
 <211> 148
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(148)
 <223> Xaa = Any Amino Acid

<400> 377
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 35 40 45
 Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
 50 55 60
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
 65 70 75 80
 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
 85 90 95
 Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
 100 105 110
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
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 Lys Leu Met Ala Lys Ala Leu Leu Tyr Gly Ala Asp Ile Glu Ser
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 Lys Asn Lys Val
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<210> 378
 <211> 1719
 <212> PRT
 <213> Homo sapien

<400> 378
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 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn

				85					90					95			
Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser		
			100					105					110				
Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe		
		115					120					125					
Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His		
	130					135					140						
Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met		
145					150					155					160		
Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala		
			165						170						175		
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Lys	Leu	Leu		
	180							185					190				
Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr		
	195						200					205					
Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu	Cys	Ala	Leu	Met		
	210					215					220						
Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn		
225				230						235					240		
Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	Leu	Met	Ala	Lys		
			245						250						255		
Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	Asn	Lys	His	Gly		
	260						265						270				
Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	Gln	Gln	Val	Val		
	275						280					285					
Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala	Leu	Asp	Arg	Tyr		
	290					295					300						
Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Ser	Ile		
305				310					315						320		
Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	Ser	Gln	Asp	Leu		
			325						330					335			
Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser	His	His	His	Val		
			340					345					350				
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile		
	355						360					365					
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Asn	Val	Ser	Arg	Thr	Arg	Asn	Lys		
	370				375						380						
Pro	Arg	Thr	His	Met	Val	Val	Glu	Val	Asp	Ser	Met	Pro	Ala	Ala	Ser		
385				390						395					400		
Ser																	

Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp
 530 535 540
 Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln
 545 550 555 560
 Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val
 565 570 575
 Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn
 580 585 590
 Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu
 595 600 605
 Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp
 610 615 620
 Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys
 625 630 635 640
 Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys
 645 650 655
 Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
 660 665 670
 Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
 675 680 685
 Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
 690 695 700
 Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
 705 710 715 720
 Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser
 725 730 735
 His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln
 740 745 750
 Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys
 755 760 765
 Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser
 770 775 780
 Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp
 785 790 795 800
 Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly
 805 810 815
 Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn
 820 825 830
 Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe
 835 840 845
 Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser
 850 855 860
 Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn
 865 870 875 880
 Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu
 885 890 895
 Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile
 900 905 910
 Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn
 915 920 925
 Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro
 930 935 940
 Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu
 945 950 955 960
 Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe

	965		970		975
Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His					
	980		985		990
Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser					
	995		1000		1005
Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu					
	1010		1015		1020
Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His					
	1025		1030		1035
Gln Ser Gln Leu Pro Arg Thr His Met Val Val Glu Val Asp Ser Met					
	1045		1050		1055
Pro Ala Ala Ser Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met					
	1060		1065		1070
Gly Lys Trp Cys Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys					
	1075		1080		1085
Ser Asn Val Gly Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr					
	1090		1095		1100
Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys					
	1105		1110		1115
Arg Gly Ser Gly Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp					
	1125		1130		1135
Ser Ala Met Lys Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His					
	1140		1145		1150
Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp					
	1155		1160		1165
Gly Asp Tyr Asp Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg					
	1170		1175		1180
Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val					
	1185		1190		1195
Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys					
	1205		1210		1215
Lys Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly					
	1220		1225		1230
Asn Ser Glu Val Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn					
	1235		1240		1245
Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys					
	1250		1255		1260
Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro					
	1265		1270		1275
Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr					
	1285		1290		1295
Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp					
	1300		1305		1310
Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val					
	1315		1320		1325
His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala					
	1330		1335		1340
Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala					
	1345		1350		1355
Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn					
	1365		1370		1375
Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr					
	1380		1385		1390
Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr					
	1395		1400		1405

Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu
 1410 1415 1420
 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly
 1425 1430 1435 144
 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn
 1445 1450 1455
 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser
 1460 1465 1470
 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly
 1475 1480 1485
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu
 1490 1495 1500
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys
 1505 1510 1515 152
 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser
 1525 1530 1535
 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu
 1540 1545 1550
 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser
 1555 1560 1565
 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe
 1570 1575 1580
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe
 1585 1590 1595 160
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly
 1605 1610 1615
 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro
 1620 1625 1630
 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln
 1635 1640 1645
 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile
 1650 1655 1660
 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser
 1665 1670 1675 168
 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn
 1685 1690 1695
 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr
 1700 1705 1710
 Met Lys His Gln Ser Gln Leu
 1715

<210> 379

<211> 656

<212> PRT

<213> Homo sapien

<400> 379

Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
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 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60

Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
 420 425 430
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
 435 440 445
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
 450 455 460
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
 465 470 475 480
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
 485 490 495
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu

Asn	Gly	Gln	500	Pro	Glu	Leu	Glu	Asn	505	Phe	Met	Ala	Ile	Glu	510	Glu	Met	Lys
		515							520						525			
Lys	His	Gly	Ser	Thr	His	Val	Gly	Phe	Pro	Glu	Asn	Leu	Thr	Asn	Gly			
	530					535							540					
Ala	Thr	Ala	Gly	Asn	Gly	Asp	Asp	Gly	Leu	Ile	Pro	Pro	Arg	Lys	Ser			
545					550					555					560			
Arg	Thr	Pro	Glu	Ser	Gln	Gln	Phe	Pro	Asp	Thr	Glu	Asn	Glu	Glu	Tyr			
			565						570					575				
His	Ser	Asp	Glu	Gln	Asn	Asp	Thr	Gln	Lys	Gln	Phe	Cys	Glu	Glu	Gln			
		580						585					590					
Asn	Thr	Gly	Ile	Leu	His	Asp	Glu	Ile	Leu	Ile	His	Glu	Glu	Lys	Gln			
	595						600						605					
Ile	Glu	Val	Val	Glu	Lys	Met	Asn	Ser	Glu	Leu	Ser	Leu	Ser	Cys	Lys			
	610					615							620					
Lys	Glu	Lys	Asp	Ile	Leu	His	Glu	Asn	Ser	Thr	Leu	Arg	Glu	Glu	Ile			
625					630					635					640			
Ala	Met	Leu	Arg	Leu	Glu	Leu	Asp	Thr	Met	Lys	His	Gln	Ser	Gln	Leu			
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<210> 380

<211> 671

<212> PRT

<213> Homo sapien

<400> 380

Met	Val	Val	Glu	Val	Asp	Ser	Met	Pro	Ala	Ala	Ser	Ser	Val	Lys	Lys			
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Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys	Cys	Arg	Cys	Phe			
			20					25					30					
Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly	Thr	Ser	Gly	Asp			
		35					40					45						
His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp			
	50					55					60							
Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	Lys	Ser	Asn	Val			
65				70					75					80				
Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Asn			
			85						90					95				
Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser			
		100						105					110					
Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe			
	115						120					125						
Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His			
	130					135					140							
Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met			
145					150					155				160				
Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala			
			165						170					175				
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Lys	Leu	Leu			
		180					185						190					
Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr			
	195						200					205						
Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu	Cys	Ala	Leu	Met			
	210					215					220							
Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn			

225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
 420 425 430
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
 435 440 445
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
 450 455 460
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
 465 470 475 480
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
 485 490 495
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
 500 505 510
 Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp
 515 520 525
 Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys
 530 535 540
 His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly Ala
 545 550 555 560
 Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser Arg
 565 570 575
 Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr His
 580 585 590
 Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn
 595 600 605
 Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile
 610 615 620
 Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys
 625 630 635 640
 Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala
 645 650 655
 Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
 660 665 670

<210> 381
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 381
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 ccaatatccc aggagaagca ttggggaggt gggggcaggt gaaggacca ggactcacac 180
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 caagcagtca g 251

<210> 382
 <211> 3279
 <212> DNA
 <213> Homo sapiens

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 cactgggagg ggacatcctg cagaaggtag gagtgagcaa acacccgctg caggggaggg 180
 gagagccctg cggcacctgg gggagcagag ggagcagcac ctgcccaggc ctgggaggag 240
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tgaagtcctc agacctgagg ttccctagag ttcaaacaga tacagcatgg tccagagtcc 2400
cagatgtaca aaaacagggg ttcatcacaa atcccatctt tagcatgaag ggtctggcat 2460
ggcccaaggc cccaagtata tcaaggcact tgggcagaac atgccaagga atcaaagtgc 2520
atctcccagg agttattcaa ggggtgagccc tttacttggg atgtacaggc tttgagcagt 2580
gcagggtctg tgagtcaacc ttttattgta caggggatga gggaaagggg gaggatgagg 2640
aagccccctt ggggatttgg tttggtcttg tgatcaggtg gtctatgggg ctatccctac 2700
aaagaagaat ccagaaatag gggcacattg aggaatgata ctgagcccaa agagcattca 2760
atcattgttt tatttgcctt cttttcacac cattggtgag ggagggatta ccaccctggg 2820
gttatgaaga tggttgaaca cccacacat agcaccggag atatgagatc aacagtttct 2880
tagccataga gattcacagc ccagagcagg aggacgctgc acaccatgca ggatgacatg 2940
ggggatgcgc tcgggatttg tgtgaagaag caaggactgt tagaggcagg ctttatagta 3000
acaagacggg ggggcaaact ctgatttccg tgggggaatg tcatggtctt gctttactaa 3060
gttttgagac tggcaggtag tgaaactcat taggctgaga accttgtgga atgcagctga 3120
cccagctgat agaggaagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
ggcaagattt tgtggcactc ctggttacag atactggggc agcaaataaa actgaatctt 3240
gttttcagac ctaaaaaaaa aaaaaaaaaa aaaagtttt 3279

```

<210> 383

<211> 155

<212> PRT

<213> Homo sapiens

<400> 383

```

Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr
          5              10              15

```

```

Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
          20              25              30

```

```

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
          35              40              45

```

```

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
          50              55              60

```

```

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
          65              70              75              80

```

```

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
          85              90              95

```

```

Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
          100              105              110

```

```

Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
          115              120              125

```

```

Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
          130              135              140

```

```

Ala Leu Glu Arg Gly His Leu Val Arg Glu
          145              150

```

<210> 384
 <211> 557
 <212> DNA
 <213> Homo sapiens

<400> 384
 ggatcctcta gagcgccgc ctactactac taaattcgcg gccgcgtcga cgaagaagag 60
 aaagatgtgt tttgttttgg actctctgtg gtcccttcca atgctgtggg ttccaacca 120
 ggggaagggt ccccttttga ttgccaagt ccataaccat gagcactact ctaccatgg 180
 tctgcctect ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240
 acttaacctt gaaatggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300
 ctctgtagag agcagcattc ccagggaact tggaaacagt tggcactgta aggtgcttgc 360
 tccccaagac acatcctaaa aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc 420
 ccttcttatt tatgtgaaca actgtttgtc tttttttgta ttttttttaa actgtaaagt 480
 tcaattgtga aaatgaatat catgcaaata aattatgoga tttttttttc aaagtaaaaa 540
 aaaaaaaaaa aaaaaaa 557

<210> 385
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 385
 ttcccagggtg atgtgcgagg gaagacacat ttactatcct tgatggggct gatcccttta 60
 gtttctctag cagcagatgg gttaggagga agtgaeccaa gtggttgact cctatgtgca 120
 tctcaaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180
 aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacctag 240
 tatcagacag gtccagtttc cgcaccaaca cctgctgggt ccctgtcgtg gtctggatct 300
 ctttggccac caattcccc ttttccacat cccggca 337

<210> 386
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 386
 gggcccgtga ccggccocagg ccccgccctcg cgagtctctc tcccccgggtg cctgcccgc 60
 gcccgctcgg cccagagggt gggcgcgggg ctgcctctac cggctggcgg ctgtaactca 120
 gcgaccttgg cccgaaggct ctagcaagga ccacccgacc ccagccgagg cggcgggcggc 180
 gcggactttrg cccggtgtgt gggcgggagc ggactgcgtg tccgaggacg ggcagcgaag 240
 atgttagcct tcgctgccag gaccgtggac cgateccagg gctgtgggtg aaacctagcc 300

<210> 387
 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 387
 gggccgagtc gggcaccaag ggactctttg caggettcct tcctcggatc atcaaggctg 60
 cccctccttg tgocatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120
 tgaaccagga ccggcttctg ggcgggtgaa aggggcaagg aggcaaggac cccgtctctc 180
 ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttcctc agcactgagg 240
 gagggggcct gtttcccttc cctccccgcg acaagctcca gggcagggtg gtccctctg 300

```

gcggcccagc acttcctcag acacaacttc ttcttgetgc tccagtcgtg gggatcatca 360
cttaccacc cccaagttc aagaccaaag cttccagctg ccccttcgt gtttccctgt 420
gtttgctgta gctgggcatg tctccaggaa ccaagaagcc ctcagcctgg tgtagtctcc 480
ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaaa aaaaaaa 537

```

<210> 388

<211> 520

<212> DNA

<213> Homo sapiens

<400> 388

```

aggataattt ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60
tgagggttaaa ccagtttgca ttcccctaag gtggaaaaag taagaggact actcagcact 120
gtttgaagat tgccctctct acagcttctg agaatttgtt tatttcactt gccaaagtga 180
ggacccccct cccaacatgc cccagcccac ccctaagcat ggtcccttgt caccaggcaa 240
ccaggaaact gctacttgtg gacctcacca gagaccagga gggtttggtt agctcacagg 300
acttccccca cccagaaga ttagcatccc atactagact cataactcaac tcaactaggc 360
tcatactcaa ttgatgggta ttagacaatt ccatttcttt ctgggtatta taaacagaaa 420
atctttcctc ttctcattac cagtaaaggc tcttggtatc tttctgttgg aatgatttct 480
atgaacttgt ctatttttaa tgggtgggtt tttttctggt 520

```

<210> 389

<211> 365

<212> DNA

<213> Homo sapiens

<400> 389

```

cggtgccccca gtttgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60
gagttaaggc tggatttcag atctgcctgg ttccagccgc agtgtgccct ctgctcccc 120
aacgactttc caaataatct caccagcgcc ttccagctca ggcgtcctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctcaccgc ctgtcctcac agctgagact 240
cccaggaaac cttcagacta ccttcctctg ccttcagcaa ggggcgttgc ccacattctc 300
tgagggtcag tggaagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360
gggag 365

```

<210> 390

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(221)

<223> n = A,T,C or G

<400> 390

```

tgccctctcca tcctggcccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60
tacacggntt ctcatgggtg tggaacatct ctgcttgagg ttccaggaag gcctctggct 120
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaaagg cggagcttat 180
tcaaagtcta gagggagtgg aggagttaag gctggatttc a 221

```

<210> 391

<211> 325

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(325)
 <223> n = A,T,C or G

<400> 391
 tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60
 ctctcgccgc cagcctggag ctgctcctgg catctaocaa caatcagncg aggcgagcag 120
 tagccagggc actgctgcc aacagccagtc cnnataccat catgtnaccc ggtgngctct 180
 naantngat ntccanagcc ctacccatcn tagttctgct ctcccacccg ntaccagccc 240
 cactgccag gaatcctaca gccagtaacc tgtcccgcag tctctaccta ccagtaacgat 300
 gagacctccg gctactacta tgacc 325

<210> 392
 <211> 277
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(277)
 <223> n = A,T,C or G

<400> 392
 atattgttta actccttctt ttatatcttt taacattttc atggngaaag gttcacatct 60
 agtctcaatt ngcnagnn ctctacttg agtctcttcc ccggcctggn ccagtnghaa 120
 antaccanga accgncatgn cttaanaacn nctgggttn tgggttnntc aatgactgca 180
 tgcagtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggccc 240
 ctgaggatac agcgcgcgct cctgtgttgc tggggaa 277

<210> 393
 <211> 566
 <212> DNA
 <213> Homo sapiens

<400> 393
 actagtccag tgtggtggaa ttccgcccgc cgtcgacgga caggtcagct gtctggctca 60
 gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga tttaaattcag cctaaacgtt 120
 ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcgggca 180
 gagaaggtct agtttgtcca tcagcattat catgatatac ggactgggta cttgggtaag 240
 gaggggtcta ggagatctgt cccttttaga gacaccttac ttataatgaa gtatttggga 300
 ggggtggttt caaaagtaga aatgtcctgt attccgatga tcacccctga aacattttat 360
 catttattaa tcacccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420
 ttctgcctca atgtttactg tgcctttgtt ttgtctagtt tgtgttgggt aaaaaaaaaa 480
 cattctctgc ctgagtttta atttttgtcc aaagttattt taatctatac aattaaaagc 540
 ttttgccat caaaaaaaaa aaaaaa 566

<210> 394
 <211> 384
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature

<222> (1)...(384)

<223> n = A,T,C or G

<400> 394

```

gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
tgcaaatng gaocgggcca aggctggact gctggagcgt gtgaaggagc tacaggccna 120
gcaggaggac cgggctttaa ggagttttaa gctgagtgtc actgtagacc ccaaatacca 180
tcccaagatt atcgggagaa agggggcagt aattacccaa atccggttgg agcatgacgt 240
gaacatccag tttcctgata aggacgatgg gaaccagccc caggaccaa ttaccatcac 300
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360
tgagcagatg gtttctgagg acgt

```

384

<210> 395

<211> 399

<212> DNA

<213> Homo sapiens

<400> 395

```

ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgc 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcattcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcatctc ctactacag acctctgacc atgggacggt 360
gcagcctggt gagaccatcc aatcccaaat aaaatgcac

```

399

<210> 396

<211> 403

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(403)

<223> n = A,T,C or G

<400> 396

```

tggagttntc agtgcaaaca agccataaag cttcagtagc aaattactgt ctcacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaaa gtggatgaat aatctggata tttttcctaa aaagattcct tgaaacacat 240
taggaaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gttttagggga gggagtgagg gataaaagaa ggaaaaaaag aagagtgaga aaacctattt 360
atcaaagcag gtgctatcac tcaatgttag gccctgctct ttt

```

403

<210> 397

<211> 100

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(100)

<223> n = A,T,C or G

<400> 397

actagtnacag tgtggtggaa ttcgcgcccg cgtcgacctt naanccatct ctatagcaaa 60
 tccatccccg ctcttggttg gtnacagaat gactgacaaa 100

<210> 398

<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 398

gcggccgcgt cgacagcagt tccgccagcg ctgcgccctg ggtggggatg tgctgcacgc 60
 ccacctggac atctggaagt cagcgccctg gatgaaagag cggacttcac ctggggcgat 120
 tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180
 ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
 ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

<210> 399

<211> 298

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(298)

<223> n = A,T,C or G

<400> 399

acggagggtg aggaagcgnc cctgggatcg anaggatggg toctgncatt gaccncctcn 60
 ggggtgccng catggagcgc atgggcgcgg gcctgggcca cggcatggat cgcgtgggct 120
 ccgagatcga gcgcattggc ctggtcatgg accgcattgg ctccgtggag cgcattggct 180
 ccggcattga gcgcattggc ccgctgggccc tcgaccacat ggccctccanc attgancgca 240
 tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcattggg 298

<210> 400

<211> 548

<212> DNA

<213> Homo sapiens

<400> 400

acatcaacta ctctctcatt ttaaggatat gcagttccct tcatoecctt ttcttgcctt 60
 gtacatgtac atgtatgaaa ttctctcttc ttaccgaact ctctocacac atcacaagggt 120
 caaagaacca cacgcttaga agggtaagag ggcacocctat gaaatgaaat ggtgatttct 180
 tgagtctctt ttttccatgt ttaaggggccc atggcaggac ttagagt-tgc gagttaagac 240
 tgcagagggc tagagaatta tttcatacag gctttgaggc caccatgtc acttatcccg 300
 tataccctct caecatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360
 gttggcccc taattctggg cctttgttgt ttgttttaat tacttgggca tccaggaag 420
 ctttccagt atctcctacc atgggcccc ctcttgggat caagccctc ccaggccctg 480
 tccocagccc ctctgcccc agccacccg cttgccttgg tgctcagccc tccattggg 540
 agcaggtt 548

<210> 401
 <211> 355
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(355)
 <223> n = A,T,C or G

<400> 401
 actgtttcca tggtatgttt ctacacattg ctacctcagt gtccttgga acttagcttt 60
 tgatgtctcc aagtagtcca ccttcattta actctttgaa actgtatcat ctttgccaag 120
 taagagtggg ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180
 tataaatgaa tgtgctgaag caaagtgcc atggtggcgg cgaagaagan aaagatgtgt 240
 tttgttttg actctctgtg gtcccttcca atgctgnggg tttccaacca ggggaagggt 300
 cccttttgca ttgccaagtg ccataacccat gagcactact ctaccatggn tctgc 355

<210> 402
 <211> 407
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(407)
 <223> n = A,T,C or G

<400> 402
 atggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60
 tctcacatgc ggtggcatac ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120
 aaatggaaaa cagaaaaaag caggtgttgc actcctactt tctgacaaaa cagactatgc 180
 gaataaagat aaaaaagaga aggacattac aaaggtgggc ctgacctttg ataaatctca 240
 ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300
 ttgtggagct tctccctgc agagagtccc tgatctccca aaatttggtt gagatgtaag 360
 gntgattttg ctgacaactc cttttctgaa gttttactca ttccaa 407

<210> 403
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(303)
 <223> n = A,T,C or G

<400> 403
 cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaatac aggcacacaaa 60
 tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120
 tagagaacaa gacctactca gtcataaaca aaaaggcaga caccaacatg gatctcatgg 180
 gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240
 tcttaacaac gaccgaaacc cattattttac ataaacctcc attcggtaac catgttgaaa 300
 gga 303

<210> 404
 <211> 225
 <212> DNA
 <213> Homo sapiens

<400> 404
 aagtgttaact tttaaaaaatt tagtggattt tgaaaaattct tagaggaaaag taaaggaaaa 60
 attgttaatg cactcattta cctttacatg gtgaaagttc tctcttgatc ctacaaacag 120
 acattttcca ctctgtgttc catagttgtt aagtgtatca gatgtgttg gcatgtgaat 180
 ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225

<210> 405
 <211> 334
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (334)
 <223> n = A,T,C or G

<400> 405
 gagctgttat actgtgagtt ctactaggaa atcatcaaatt ctgagggttg tctggaggac 60
 ttcaatacac ctccccccat agtgaatcag cttccagggg gtccagtcct tctccttact 120
 tcatcccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctaggc 180
 ttcccagtg ctcaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtg 240
 ctggtgcggt tgtgctcca gcttctgctc agtgcttcat ggacagtgc cagcccatgt 300
 cactctccac tctctcannn tggatcccac ccct 334

<210> 406
 <211> 216
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1) ... (216)
 <223> n = A,T,C or G

<400> 406
 tttcatacct aatgagggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60
 gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
 acnaaacaca aatttntatgt tgcaccccttg tttctacacc tgtgggttat gacaaagaca 180
 actgccaaaag aatnttcaag aaggaggact gccant 216

<210> 407
 <211> 413
 <212> DNA
 <213> Homo sapiens

<400> 407
 gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60
 gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120
 gtacaacatt gcacccagtg tcagattcta cacctggcca cttaggaagc aagagttaat 180
 ccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240

```

ggaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt tttcctgtca 360
tgggagttcc agaaaaagtt aaaacagaca atgggccagg ttctgtagta aag          413

```

```

<210> 408
<211> 183
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(183)
<223> n = A,T,C or G

```

```

<400> 408
ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttggnattaa 60
tnccttaacta gttaatcctt aaagggctan ntaatcctta actagtcctt ccattgtgag 120
cattatcctt ccagtattcn ccttctnttt tatttactcc ttctgggcta cccatgtact 180
ntt                                     183

```

```

<210> 409
<211> 250
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(250)
<223> n = A,T,C or G

```

```

<400> 409
cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60
gtggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180
gcttccagtg gccccagga cagcgtgggc tatgtttaca gcgcntcctt gctggggggg 240
ggccntatgc                                     250

```

```

<210> 410
<211> 306
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(306)
<223> n = A,T,C or G

```

```

<400> 410
ggctgggttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
agtcttgcaa tccatttgc aggatecgtc tgtgcacatg cctctgtaga gagcagcatt 120
cccagggacc ttggaaacag ttggcactgt aaggtgcttg ctecccaaga cacatcctaa 180
aaggtgttgt aatggtgaaa accgcttcc tctttattgc cccttcttat ttatgtgaac 240
nactggttgg ctttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300
tcntgc                                     306

```

<210> 411
<211> 261
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (261)
<223> n = A,T,C or G

<400> 411
agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaagtgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa gngaggcaa a 261

<210> 412
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (241)
<223> n = A,T,C or G

<400> 412
gttcaatgtt acctgacatt tctacaacac cccactcacc gatgtattcg ttgccagtg 60
ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgccagg aaatactacg 120
actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180
ctgggagatt tcactgggta cattgaattc ccaaaactacc cangcaatta ccagccaac 240
a 241

<210> 413
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (231)
<223> n = A,T,C or G

<400> 413
aactcttaca atocaagtga ctcactctgtg tgcttgaatc cttbcaactg tctcatctcc 60
ctcatccaag ttcttagtac cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120
aagtttactc tcctcatattg gaacctaaaa actctcttct tcctgggtct gagggctcca 180
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

<210> 414
<211> 234
<212> DNA
<213> Homo sapiens

<400> 414

actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
 gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
 gtgagccaag gagggagggt cttcctttgg catgggatgg ggatgaagta aggagagggg 180
 ctggaccccc tggaagctga ttcactatgg ggggaggtgt attgaagtcc tcca 234

<210> 415

<211> 217

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (217)

<223> n = A,T,C or G

<400> 415

gcataggatt aagactgagt atcttttcta cattctttta acttttctaag gggcacttct 60
 caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cacttttctca 120
 cacctagcaa tagtagaatt cagtcctact tctgaggcca gaagaatggt tcagaaaaat 180
 antggattat aaaaaataac aattaagaaa aataatc 217

<210> 416

<211> 213

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (213)

<223> n = A,T,C or G

<400> 416

atgcatatnt aaagganact gcctcgcttt tagaagacat ctggngctgct ctctgcatga 60
 ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120
 cgaatgcaag gtgggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180
 atattggaac agatggagtc tctactacaa aag 213

<210> 417

<211> 303

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (303)

<223> n = A,T,C or G

<400> 417

nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60
 gtgggaaagg ctttactctg agttcaaadc ttcaagccca tcagagagtc cactactggag 120
 agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180
 ttcatttagt ggtccacaca ggagagaaac cctataaatg tgagatatgt ggggaagggt 240
 tcantcaaag ttcgtatctt caaatccatc ngaaggncca cagtatanan aaacctttta 300
 agt 303

<210> 418
<211> 328
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

<400> 418
tttttggcgg tgggtggggca gggacggggac angagtctca ctctgttgcc caggctggag 60
tgcacaggca tgatctcggc tcactacaac ccctgcctcc catgtccaag cgattcttgt 120
gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacaccca gctagttttt 180
gtatttttag tagagacagg gtttcaccat gttggccagg ctggtctcaa actcctnacc 240
tcagnggtca ggctgggtctc aaactcctga cctcaagtga tctgcccacc tcagcctccc 300
aaagtgctan gattacagggc cgtgagcc 328

<210> 419
<211> 389
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(389)
<223> n = A,T,C or G

<400> 419
cctcctcaag acggcctgtg gtccgcctcc eggcaaccaa gaagcctgca gtgccatattg 60
acccctgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120
cttgtttccct ctctgtggct ccattcatag cacagtgtgt gcactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggt gtgccaggca 240
ccggttctcc agccaccaac ctactcgtc cccgcaaatt gcacatcagt tcttctaacc 300
taaaggtagg accaaagggc atctgctttt ctgaagtcc ctgctctatc agccatcaag 360
tggcagccac tcnggctgtg tcgaagcgg 389

<210> 420
<211> 408
<212> DNA
<213> Homo sapiens

<400> 420
gttcctccta actcctgcc aaaaacagctc tcttcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggtc tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttggcat ggagaacgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgtatg acaaaccctg caagcgcg 408

<210> 421
<211> 352
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(352)

<223> n = A,T,C or G

<400> 421

```
gctcaaaaat ctttttactg atnggcatgg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacaggtct tttttgggtc cttcttctcc accacnatat acttgagtc 180
ctccttcttg aagattcttt ggcagttgtc ttgtcataa cccacaggtg tagaaacaag 240
ggtgcaacat gaaatttctg tttcgtagca agtgcattgc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttcct gg 352
```

<210> 422

<211> 337

<212> DNA

<213> Homo sapiens

<400> 422

```
atgccaccat gctggcaatg cagcggggcg tccaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgcgatgcc agccgaagcg gtggtcaagg 120
gcgatagcaa ggtgccggcg atcgcgggcg cgtcaatcct ggccaaggct agccgtgatc 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcgggcgg cataagggtc 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
gcttcttccg ccggtacggc tggcctatga aaattat 337
```

<210> 423

<211> 310

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(310)

<223> n = A,T,C or G

<400> 423

```
gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
aggagaatga ggccctggcc tgggagccct tgcctactan aagcncatta gattatccat 120
tcactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtcc 180
tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240
gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgcc 300
tccgagttta 310
```

<210> 424

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(370)

<223> n = A,T,C or G

<400> 424
gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120
cactgacaga acaggtcttt tttgggtcct tcttctccac cacgatatac ttgcagtctt 180
ccttcttgaa gattctttgg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240
ggttgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300
cacgaagggtg gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
tccgtcgcagc 370

<210> 425
<211> 216
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(216)
<223> n = A,T,C or G

<400> 425
aattgctatn ntatttttg ccactcaaaa taattacca aaaaaaaaaa tnttaaataga 60
taacaacnca acatcaagg aaananaaca ggaatggntg acntgcata aatnggccga 120
anattatcca ttatnttaag gggtgacttc aggntacagc acacagacaa acatgcccg 180
gaggntntca ggaccgctcg atgtntntg aggagg 216

<210> 426
<211> 596
<212> DNA
<213> Homo sapiens

<400> 426
cttcagtgga ggataaccct gttgccccgg gccgaggttc tccattaggc tctgattgat 60
tggcagtcag tgatggaagg gtgttctgat cattccgact gcccacaagg tcgctggcca 120
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatggtga 180
gctgtccttg tattttgatt aaocctaatgg octtcccagc acgactcgga ttcagctgga 240
gacatcacgg caacttttaa tgaaatgatt tgaagggcca ttaagaggca ctccccgtta 300
ttaggcagtt catctgcact gataacttct tggcagctga gctggtcgga gctgtggccc 360
aaacgcacac ttggcttttg gtttgagat acaactctta atcttttagt catgcttgag 420
gggtggatggc cttttcagct ttaacccaat ttgcactgcc ttggaagtgt agccaggaga 480
atacactcat atactcgtgg gcttagaggc cacagcagat gtcattgggt tactgcctga 540
gtcccgtggt tcccatccca ggacctoca tggcgagta cctgggagcc cgtgct 596

<210> 427
<211> 107
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(107)
<223> n = A,T,C or G

<400> 427
gaagaattca agttaggttt attcaaaggg cttacngaga atcctanacc caggncocag 60

cccgggagca gccttanaga gctcctgttt gactgccccg ctcagn

107

<210> 428

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(38)

<223> n = A,T,C or G

<400> 428

gaacttcna anaangactt tattcactat ttacatt

38

<210> 429

<211> 544

<212> DNA

<213> Homo sapiens

<400> 429

ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60
 attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
 atatccacga actcttgaag gactttctga tttatccaca atcaaatacat cggttttcag 180
 tttggatggt ggctcatcac ctgtagaacc tgacttgccc gtggctggaa tccactcgtt 240
 gccttccact tcagttacac ctcaactcacc atctctctct gttgggttctg tgctgcttca 300
 agatactaag cccacatttg agatgcagca gccatctccc ccaattctct ctgtccatcc 360
 tgatgtgcag ttaaaaaatc tgccttttta tgatgtcctt gatgttctca tcaagcccac 420
 gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
 acctcaacaa gttagagaga tatgcatatc cagggatttt ttgccaggtg gtaggagaga 540
 ttat 544

<210> 430

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(507)

<223> n = A,T,C or G

<400> 430

cttatcncaa tggggctccc aaacttggct gtgcagtgga aactccgggg gaattttgaa 60
 gaacactgac acccatcttc caccocgaca ctctgattta attgggctgc agtgagaaca 120
 gagcatcaat ttaaaaagct gcccagaatg ttntcctggg cagcgttggt atctttgccc 180
 ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgaggga gttccaggag 240
 attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
 caagaaggag gactgcaagt atatcgtggg ggagaagaag gacccaaaaa agacctgttc 360
 tgtcagttaa tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420
 cattctcctc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480
 ttttgagcaa aaaaaaaaaa aaaaaaa 507

<210> 431

<211> 392

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (392)

<223> n = A,T,C or G

<400> 431

```

gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagogat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtectgggtt ttccaacaga 240
catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tgttgttagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360
gcaatgagtc tggctttttac tctgctgttt ct 392

```

<210> 432

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (387)

<223> n = A,T,C or G

<400> 432

```

ggtatccnta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtccaa gctctcggna gtccagccac tngaaacat gctcccttta gattaacctc 180
gtggacnctn ttgttgnatt gtctgaactg tagngccctg tatttttgctt ctgtctgnga 240
attctgttgc ttctggggca ttctcttngn atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtac aggaccggga 360
acaacgtata gaacactgga gtccttt 387

```

<210> 433

<211> 281

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (281)

<223> n = A,T,C or G

<400> 433

```

ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc accgagttat 60
ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattccctn ttgntattac accagngagg ntctctgtnt gcccaactgg 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281

```

<210> 434

<211> 484

<212> DNA

<213> Homo sapiens

<400> 434

```
ttttaaaata agcatttagt gctcagtcct tactgagtac tctttctctc ccctcctctg 60
aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatattg 120
tggtgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtaga tccatcttgc 180
tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acaggtgaat tggatgggtc tcagaacccat ttcacccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaaccc 360
tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag tacccatgtc 480
ttta
```

484

<210> 435

<211> 424

<212> DNA

<213> Homo sapiens

<400> 435

```
gcgccgctca gagcagggtca ctttctgcct tccacgtcct ccttcaagga agccccatgt 60
gggtagcttt caatatcgca ggttcttact cctctgcctc tataagctca aaccaccaa 120
cgatcgggca agtaaaccct ctccctcgcc gacttcggaa ctggcgagag ttcagcgag 180
atgggctgtt ggggaggggg caagatagat gagggggagc ggcatggtgc ggggtgacc 240
cttgagaga ggaaaaggc cacaagagg gctgccaccg ccactaacgg agatggcct 300
ggtagagacc tttgggggtc tggaacctct ggactccca tgccttaact cccacactct 360
gctatcagaa acttaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac
```

424

<210> 436

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (667)

<223> n = A,T,C or G

<400> 436

```
accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataagggtgc 120
agcctcttct ggaattcctc tgatttcaaa gtctcactct caagttcttg aaaacgaggg 180
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacaggggt 300
gccaggtttg tcatagcact catcaaagtc cgggtcaacgt ctgtgcttcg aatataaacc 360
tgttcatgtt tataggactc attcaagaat tttctatata tctttcttat atactctcca 420
agttcataat gctgctccat gccagctgg gtgagttggc caaatccttg tggccatgag 480
gattccttta tggggctcag gggaaagggt tcaatgggac ttcgggtctcc atgccgaaac 540
accaaagtca caaacttcaa ctcttgggt agtacacttc ggtctagcca gaaaaaaagc 600
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660
tgttgag
```

667

<210> 437

<211> 693

<212> DNA

<213> Homo sapiens

<400> 437

```

ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaag ctggattggc acactaggac tctaccatac cgggttttgt 120
taaagctcag gttaggaggc tgataagctt ggaaggaaact tcagacagct ttttcagatc 180
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtactcct ctattttcac ccctcttgct tctactctct ggagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatggt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttgggggggac agccagcatc tttagctttc 420
atgtgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaaact gctgttgctc ctgaggtggt gaaagacaga tatagagctt acagtattta 540
tcctattttct aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc
693

```

<210> 438

<211> 360

<212> DNA

<213> Homo sapiens

<400> 438

```

ctgcttatca caatgaatgt tctcctgggc agcgttggtga tctttgccac ctctgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgagggag ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaag acaactgcc aagaatcttc aagaaggagg 180
actgcaagta tatctgggtg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccag ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360

```

<210> 439

<211> 431

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (431)

<223> n = A,T,C or G

<400> 439

```

gttcctnnta actcctgcc a gaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tgccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaocgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgctcg cgcggcccg 420
aatttagtag t
431

```

<210> 440

<211> 523

<212> DNA

<213> Homo sapiens

<400> 440

```

agagataaag cttagggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaagtgc tgaaatggaa cagattttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagtccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tcctggaaca tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaat acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcatctga tgagaacaag cta 523

```

<210> 441

<211> 430

<212> DNA

<213> Homo sapiens

<400> 441

```

gttcctccta actcctgcc aaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggg gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaaac ctcattggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag 430

```

<210> 442

<211> 362

<212> DNA

<213> Homo sapiens

<400> 442

```

ctaaggaatt agtagtggtc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcctggaa tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attaagctat 180
atgttttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc 362

```

<210> 443

<211> 624

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(624)

<223> n = A,T,C or G

<400> 443

```

tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60
ttgaaagaat taaattcaga ggaggggaga gaaagagtac tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240

```



```

cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggg ttaaataaac 360
taacgcctac aaaacactta aacatagata acataggtgc aagtactatg tatctggtag 420
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaata 480
agtacagaga gagggcactt aaaccaacta agggcctgga ggggaagggtt cctggaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600
ttgtccctat ctgctaataa gatc 624

```

```

<210> 444
<211> 425
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(425)
<223> n = A,T,C or G

```

```

<400> 444
gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtgggtg gtcagcaaat ccttgaatgc 180
tgcttaattg gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttggttt tgcatcctgt gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggtcgacg cggccgcgaa tttagtagta 420
gtaga 425

```

```

<210> 445
<211> 414
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(414)
<223> n = A,T,C or G

```

```

<400> 445
catgtttatg nttttggatt actttgggca octagtgttt ctaaatcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcatgtggc agattattgg atgtagtttc ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtgggtggaa ttaaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggcctctcc tcttgtattt tgaagcagtg 360
tggtgtctgg attgataaaa aaaaaaaaaa tgcacgcggc cgogaattta gtag 414

```

```

<210> 446
<211> 631
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(631)

```

<223> n = A,T,C or G

<400> 446

```
acaaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcaggtgtg 120
atgctggtta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180
ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtggtgggc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagattt gtaaaactttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatggt tcacagtggc tggactaccg agagcttgga ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tggtgccttg catttggtgt 540
aatctacacc aatgaaaaca tgtactacag ctatatattga ttatgtatgg atatatttga 600
aatagtatac attgtcttga tgttttttct g                                     631
```

<210> 447

<211> 585

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(585)

<223> n = A,T,C or G

<400> 447

```
ccttggggaaa antntcacaa tataaagggt cgtagacttt actccaaatt ccaaaaagggt 60
cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagttcttga aaacgagggc 180
agttcctgaa aggcagggtat agcaactgat cttcagaaaag aggaactgtg tgcaccggga 240
tggtggtgcca gaggtaggata ggattccaga tgctgacacc ttctggggga aacaggggtg 300
ccagggttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcattgtt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480
attcctttat ggggtcagtg ggaaagggtg caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggcta gtacacttcg gtcta                                     585
```

<210> 448

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(93)

<223> n = A,T,C or G

<400> 448

```
tgctegtggg tcattctgan nnccgaactg acctgcccag ccctgccgan gggccnccat 60
ggctccctag tgccctggag agganggggc tag                                     93
```

<210> 449

<211> 706

<212> DNA

<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(706)
 <223> n = A,T,C or G

<400> 449
 ccaagttcat gctntgtgct ggacgctgga caggggggcaa aagcnnttgc tcgtgggtca 60
 ttctgancac cgaactgacc atgocagccc tgcgatgggt cctccatggc tccctagtgc 120
 cctggagagg aggtgtctag tcagagagta gtccctggaag gtggcctctg ngaggagcca 180
 cggggacagc atcctgcaga tggtcggggcg cgtcccatc gccattcagg ctgcgcaact 240
 gttgggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300
 gtgctgcaag gcgattaagt tgggtaacgc caggggtttc ccagtcncga cgttgtaaaa 360
 cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcattgcacg 420
 cgtacgtaag cttggatcct ctagagcggc cgcctactac tactaaattc gcgggcgcgt 480
 cgacgtggga tccncaactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
 cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
 aacaggttga acctgggagg tggagggtgc aatgagctga gatcaggccn ctgcncccca 660
 gcatggatga cagagtgaaa ctccatctta aaaaaaaaaa aaaaaa 706

<210> 450
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 450
 gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60
 acagttttta aaggtaaaac aacataaaaa gaaatatcct atagtggaaa taagagagtc 120
 aaatgaggct gagaacttta caaagggatc ttacagacat gtcgccaata tcaactgcacg 180
 agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggracaattc 240
 caagtcagggt agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
 agagacactg tcagagagtt aaaaagttag ttctatccat gaggtgattc cacagtcttc 360
 tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
 tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggg cgacgcggcc 480
 gcgaatttag tag 493

<210> 451
 <211> 501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(501)
 <223> n = A,T,C or G

<400> 451
 gggcgcgctc cattcgecat tcaggctgcg caactgttgg gaagggcgat cgggtgcgggc 60
 ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120
 aacgccaggg ttttccagc cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180
 tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240
 gcggccgcct actactacta aattcgcggc cgcgtcgacg tgggatccnc actgagagag 300
 tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacia 360
 cgcncacagac actcacagct actcaggagg ctgagaacag gttgaacctg ggagggtggag 420
 gttgcaatga gctgagatca ggccnctgcn cccagcagat gatgacagag tgaaactoca 480

tcttaaaaaa aaaaaaaaaa a

501

<210> 452

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(51)

<223> n = A,T,C or G

<400> 452

agacggtttc accntttacaa cnccttttag gatgggnntt ggggagcaag c

51

<210> 453

<211> 317

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(317)

<223> n = A,T,C or G

<400> 453

tacatcttgc	tttttcccca	ttggaactag	tcattaaccc	atctctgaac	tggtagaaaa	60
acatctgaag	agctagtcta	tcagcatctg	gcaagtgaat	tggtatgggtc	tcagaaccat	120
ttcacccana	cagcctgttt	ctatcctgtt	taataaatta	gtttgggttc	tctacatgca	180
taacaaaccc	tgctccaatc	tgtcacataa	aagctctgtga	cttgaagttt	antcagcacc	240
cccaccaaac	tttatttttc	tatgtgtttt	ttgcaacata	tgagtgtttt	gaaaataagg	300
tacccatgtc	tttatta					317

<210> 454

<211> 231

<212> DNA

<213> Homo sapiens

<400> 454

ttcgaggtag	aatcaactct	cagagtgtag	tttccttcta	tagatgagtc	agcattaata	60
taagccacgc	cacgctcttg	aaggagtctt	gaattctcct	ctgctcactc	agtagaacca	120
agaagaccaa	attcttctgc	atcccagctt	gcaaacaaaa	ttgttcttct	aggtctccac	180
ccttcctttt	tcagtgttcc	aaagctcttc	acaatttcat	gaacaacagc	t	231

<210> 455

<211> 231

<212> DNA

<213> Homo sapiens

<400> 455

taccaaagag	ggcataataa	tcagtctcac	agtaggggttc	accatcctcc	aagtgaaaaa	60
cattgttccg	aatgggcttt	ccacaggcta	cacacacaaa	acaggaaaca	tgccaagttt	120
gtttcaacgc	attgatgact	tctccaagga	tcttcctttg	gcatcgacca	cattcagggg	180
caaagaattt	ctcatagcac	agctcacaat	acagggtctcc	tttctcctct	a	231

<210> 456
<211> 231
<212> DNA
<213> Homo sapiens

<400> 456
ttggcaggta cccttacaaa gaagacacca taccttatgc gttattaggt ggaataatca 60
ttccattcag tattatcggt attattcttg gagaaacct gtctgtttac tgtaaccttt 120
tgcactcaaa ttccctttatc aggaataact acatagccac tatttacaaa gccattggaa 180
cctttttatt tgggtgcagct gctagtcagt cctgactga cattgccaag t 231

<210> 457
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(231)
<223> n = A,T,C or G

<400> 457
cgaggtagct aggggtctga aaatctctnn ttantagtc gatagcaaaa ttgttcatca 60
gcattcctta atatgatctt gctataatta gattttcttc cattagagtt catacagttt 120
tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgatatcc 180
agttgtctaa atcgatgctt catttcctct gaggtgtcgc tggcttttgt g 231

<210> 458
<211> 231
<212> DNA
<213> Homo sapiens

<400> 458
aggtctgggt ccccccactt ccaactccct ctactctctc taggactggg ctgggccaag 60
agaagagggg tgggttagga agocgttgag acctgaagcc ccaacctcta ccttcccttca 120
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180
ggtcctgggt taggcatttt ggggggcccag accccaggag aagaagattc t 231

<210> 459
<211> 231
<212> DNA
<213> Homo sapiens

<400> 459
ggtaccgagg ctgcgtgaca cagagaaacc ccaacgcgag gaaaggaatg gccagccaca 60
ccttcgcgaa acctgtgggt gcccaaccagt cctaaccggga caggacagag agacagagca 120
gccctgcact gttttccctc caaccagacc atcctgtccc tcattggctc tgtgctttcc 180
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctcac a 231

<210> 460
<211> 231
<212> DNA
<213> Homo sapiens

<400> 460

```
gcaggtataa catgctgcaa caacagatgt gactaggaac ggccggtgac atggggaggg 60
cctatcaccc tattcttggg ggctgcttct tcacagtgat catgaagcct agcagcaaat 120
cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180
gtggagcttg gtccagcctc cagtccaccc ctaccaggct taaggataga a 231
```

<210> 461

<211> 231

<212> DNA

<213> Homo sapiens

<400> 461

```
cgagggttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggagggtc 60
gcgtgtgctc cagaagagtg tgtgcatgcc agaggggaaa caggcgcctg tgtgtcctgg 120
gtgggggttca gtgaggagtg ggaaattggt tcagcagaac caagccgttg ggtgaataag 180
agggggattc catggcactg atagagccct atagtttcag agctgggaat t 231
```

<210> 462

<211> 231

<212> DNA

<213> Homo sapiens

<400> 462

```
aggtaccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60
gggtcatgca agtataaaaa ttaaaaaaaa aagacttcat gccaatctc atatgatgtg 120
gaagaactgt tagagagacc aacagggtag tgggttagag atttcagag tcttacattt 180
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a 231
```

<210> 463

<211> 231

<212> DNA

<213> Homo sapiens

<400> 463

```
tactccagcc tggtgacaga gcgagaccct atcacccccc cccacccccc caaaaaaaaa 60
actgagtaga caggtgtcct cttggcatgg taagtcttaa gtcccctccc agatctgtga 120
catttgacag gtgtcttttc ctctggacct cgggtgtcccc atctgagtga gaaaaggcag 180
tggggagggtg gatcttccag tcgaagcggg atagaagccc gtgtgaaaag c 231
```

<210> 464

<211> 231

<212> DNA

<213> Homo sapiens

<400> 464

```
gtactctaag attttatcta agttgccttt tctgggtggg aaagtttaac cttagtgact 60
aaggacatca catatgaaga atgtttaagt tggagggtggc aacgtgaatt gcaaacaggg 120
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180
ggtgccagcg caccagctag atgctctgta acttctaggc cccattttcc c 231
```

<210> 465

<211> 231

<212> DNA

<213> Homo sapiens

<400> 465

```

catgttggtg tagctgtggt aatgctggct gcatctcaga cagggttaac ttcagctcct 60
gtggcaaatt agcaacaaat tctgacatca tatttatggt ttctgtatct ttgttgatga 120
aggatggcac aatttttgct tgtgttcata atatactcag attagttcag ctccatcaga 180
taaactggag acatgcagga cattagggta gtgttgtagc tctggtaatg a 231

```

<210> 466

<211> 231

<212> DNA

<213> Homo sapiens

<400> 466

```

caggtaacctc tttccattgg atactgtgct agcaagcatg ctctccgggg tttttttaat 60
ggccttcgaa cagaacttgc cacataccca ggtataatag tttctaacat ttgcccagga 120
cctgtgcaat caaatattgt ggagaattcc ctagctggag aagtcacaaa gactataggc 180
aataatggag accagtccca caagatgaca accagtcggt gtgtgoggct g 231

```

<210> 467

<211> 311

<212> DNA

<213> Homo sapiens

<400> 467

```

gtacaccctg gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg 60
tggcggcctt tctccttttt catcaagact cctcagcagg gagccagac cagcctgcac 120
tgtgccttaa cagaaggctc tgagattcta agtgggaatc atttcagtga ctgtcatgtg 180
gcatgggtct ctgccaaagc tctaatgag actatagcaa ggcggctgtg ggacgtcagt 240
tgtgacctgc tgggcctccc aatagactaa caggcagtg cagt.tggacc caagagaaga 300
ctgcagcaga c 311

```

<210> 468

<211> 3112

<212> DNA

<213> Homo sapiens

<400> 468

```

cattgtgttg ggagaaaaac agaggggaga tttgtgtggc tgcagccgag ggagaaccagg 60
aagatctgca tgggtgggaag gacctgatga tacagagttt gataggagac aattaaaggc 120
tgggaaggcac tggatgcctg atgatgaagt ggactttcaa actggggcac tactgaaacg 180
atgggatggc cagagacaca ggagatgagt tggagcaagc tcaataacaa agtgggttcaa 240
cgaggacttg gaattgcatg gagctggagc tgaagtttag cccaattgtt tactagttga 300
gtgaatgtgg atgattggat gatcatttct catctctgag cctcagggtt cccatccata 360
aaatgggata cacagtatga tctataaagt gggatatagt atgatctact tcaactgggtt 420
atattgaagga tgaattgaga taatttattt cagggtgcta gaacaatgcc cagattagta 480
catttggttg aactgagaaa tggcataaca ccaaatttaa tataatgtcag atgttactat 540
gattatcatt caatctcata gttttgtcat ggoccaattt atoctcactt gtgectcaac 600
aaattgaact gttaacaaag gaatctctgg tcttgggtaa tggctgagca cactgagca 660
tttocattcc agttggcttc ttgggtttgc tagctgcac actagtcac ttaataaat 720
gaagttttaa catttctcca gtgatttttt tatctcacct ttgaagatac tatgttatgt 780
gattaaataa agaacttgag aagaacaggt ttcattaaac ataaaatcaa tgtagacgca 840
aattttctgg atgggcaata cttatgttca caggaaatgc tttaaaatat gcagaagata 900
attaaatggc aatggacaaa gtgaaaaact tagacttttt tttttttttt ggaagtatct 960
ggatgttcct tagtcactta aaggagaact gaaaaatagc agtgagttcc acataatcca 1020
acctgtgaga ttaaggctct ttgtggggaa ggacaaagat ctgtaaattt acagtttctt 1080
tccaaagoca acgtcgaatt ttgaaacata tcaaagctct tcttcaagac aaataatcta 1140
tagtacatct ttcttatggg atgcacttat gaaaaatggg ggctgtcaac atctagtcac 1200

```

```

tttagctctc aaaatgggtc attttaagag aaagtttttag aatctcatat ttattcctgt 1260
ggaaggacag cattgtggct tggactttat aaggtcttta ttcaactaaa taggtgagaa 1320
ataagaaagg ctgctgactt taccatctga ggccacacat ctgctgaaat ggagataatt 1380
aacatcacta gaaacagcaa gatgacaata taatgtctaa gtatgacat gtttttgac 1440
atttccagcc cctttaaata tccacacaca caggaagcac aaaaggaagc acagagatcc 1500
ctgggagaaa tggccggccg ccatcttggtg tcatcgatga gcctcgccct gtgctggtc 1560
ccgcttgatga gggaaggaca ttagaaaatg aattgatgtg ttccttaaag gatgggcagg 1620
aaaacagatc ctgttggtga tatttatttg aacgggatta cagatttgaa atgaagtac 1680
aaagtgagca ttaccaatga gaggaaaaca gacgagaaaa tcttgatggc ttcacaagac 1740
atgcaacaaa caaaatggaa tactgtgatg acatgaggca gccaaagctgg ggaggagata 1800
accacggggc agagggtcag gattctggcc ctgctgccta aactgtgcgt tcataaccaa 1860
atcatttcat atttctaacc ctcaaaacaa agctgttgta atatctgatc tctacggttc 1920
cttctggggc caacattctc catatatcca gccacactca tttttaatat ttagttccca 1980
gatctgtact gtgacctttc tacactgtag aataacatta ctcattttgt tcaaagacc 2040
ttcgtgttg cgcctaatat gtagctgact gtttttccta aggagtgttc tggccagg 2100
gatctgtgaa caggctggga agcatctcaa gatctttcca gggttatact tactagcaca 2160
cagcatgatc attacggagt gaattatcta atcaacatca tcctcagtgt ctttgcccat 2220
actgaaattc atttccact tttgtgcccc ttctcaagac ctcaaaatgt cattccatta 2280
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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification: C12N 15/12, C07K 14/47, C12Q 1/68, A61K 39/395, G01N 33/68, 33/574, C07K 16/30, C12N 15/62, 5/02 // A61P 35/00		A3	(11) International Publication Number: WO 00/04149																					
(21) International Application Number: PCT/US99/15838		(43) International Publication Date: 27 January 2000 (27.01.00)																						
(22) International Filing Date: 14 July 1999 (14.07.99)		(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).																						
(30) Priority Data: <table border="0"> <tr> <td>09/115,453</td> <td>14 July 1998 (14.07.98)</td> <td>US</td> </tr> <tr> <td>09/116,134</td> <td>14 July 1998 (14.07.98)</td> <td>US</td> </tr> <tr> <td>09/159,822</td> <td>23 September 1998 (23.09.98)</td> <td>US</td> </tr> <tr> <td>09/159,812</td> <td>23 September 1998 (23.09.98)</td> <td>US</td> </tr> <tr> <td>09/232,880</td> <td>15 January 1999 (15.01.99)</td> <td>US</td> </tr> <tr> <td>09/232,149</td> <td>15 January 1999 (15.01.99)</td> <td>US</td> </tr> <tr> <td>09/288,946</td> <td>9 April 1999 (09.04.99)</td> <td>US</td> </tr> </table>		09/115,453	14 July 1998 (14.07.98)	US	09/116,134	14 July 1998 (14.07.98)	US	09/159,822	23 September 1998 (23.09.98)	US	09/159,812	23 September 1998 (23.09.98)	US	09/232,880	15 January 1999 (15.01.99)	US	09/232,149	15 January 1999 (15.01.99)	US	09/288,946	9 April 1999 (09.04.99)	US	(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
09/115,453	14 July 1998 (14.07.98)	US																						
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09/288,946	9 April 1999 (09.04.99)	US																						
(71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).		Published <i>With international search report.</i>																						
(72) Inventors: DILLON, Davin, Clifford; 21607 N.E. 24th Street, Redmond, WA 98053 (US). HARLOCKER, Susan, Louise; 6203 20th Avenue N.W., Seattle, WA 98107 (US). YUQIU, Jiang; 5001 South 232nd Street, Kent, WA 98032 (US). XU, Jiangchun; 15805 S.E. 43rd Place, Bellevue, WA 98006 (US). MITCHAM, Jennifer, Lynn; 16677 Northeast 88th Street, Redmond, WA 98052 (US).		(88) Date of publication of the international search report: 20 July 2000 (20.07.00)																						
(54) Title: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER																								
(57) Abstract Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate tumor protein, or mRNA encoding such a protein, in a sample are also provided.																								

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DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

INTERNATIONAL SEARCH REPORT

International Application No

PCT/JS 99/15838

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/47 C12Q1/68 A61K39/395 G01N33/68
G01N33/574 C07K16/30 C12N15/62 C12N5/02
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According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 97 33909 A (CORIXA CORP) 18 September 1997 (1997-09-18) the whole document	1-22, 29-31, 35-49, 53-79
A	SJOGREN H O: "Therapeutic immunization against cancer antigens using genetically engineered cells" IMMUNOTECHNOLOGY, vol. 3, no. 3, 1 October 1997 (1997-10-01), pages 161-172, XP004097000 ISSN: 1380-2933 the whole document --- -/--	23-28, 32-34, 53-57

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- *Z* document member of the same patent family

Date of the actual completion of the international search

31 January 2000

Date of mailing of the international search report

04.05.00

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

ANDRES S.M.

INTERNATIONAL SEARCH REPORT

International Application No

PCT, JS 99/15838

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>CHU R S ET AL: "CPG OLIGODEOXYNUCLEOTIDES ACT AS ADJUVANTS THAT SWITCH ON T HELPER 1 (TH1) IMMUNITY"</p> <p>JOURNAL OF EXPERIMENTAL MEDICINE, vol. 186, no. 10, 1 November 1997 (1997-11-01), pages 1623-1631, XP002910130 ISSN: 0022-1007 the whole document</p> <p>---</p>	14-20, 25-27, 41-47
A	<p>EP 0 317 141 A (BECTON DICKINSON CO) 24 May 1989 (1989-05-24) the whole document</p> <p>---</p>	50-52
A	<p>ZITVOGEL L ET AL: "Eradication of established murine tumors using a novel cell-free vaccine: dendritic cell-derived exosomes"</p> <p>NATURE MEDICINE, vol. 4, no. 5, 1 May 1998 (1998-05-01), pages 594-600, XP002085387 ISSN: 1078-8956 cited in the application</p> <p>---</p>	
P,X	<p>WO 98 37093 A (CORIXA CORP) 27 August 1998 (1998-08-27)</p> <p>page 3, line 20 -page 22, line 2 page 35, line 9 - last line page 76, line 34 -page 78, line 22 claims</p> <p>---</p>	1-15, 17-19, 21,22, 29-31, 34,35, 39-42, 44-46, 48,49, 58-79
P,X	<p>WO 98 37418 A (CORIXA CORP) 27 August 1998 (1998-08-27)</p> <p>page 2 -page 24 example 2 page 35, line 15 -page 36, line 11 page 81, line 14 -page 83, line 11 claims</p> <p>-----</p>	1-15, 17-19, 21,22, 29-31, 34,35, 39-42, 44-46, 48,49, 58-79

INTERNATIONAL SEARCH REPORT

In ternational application No.

PCT/US 99/ 15838

Box I Observations where certain claim were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claim under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 29-34, 48-49, 52, 55-57
are directed to a method of treatment of the human/animal
body, the search has been carried out and based on the alleged
effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such
an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all
searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment
of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report
covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is
restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-79 all partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

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Invention 1. Claims: 1-79 (all partially)

A polypeptide comprising at least an immunogenic portion of a prostate tumor protein defined as SEQ ID 108 and which is encoded by the related SEQ IDs 2,3,107 (according to the Description of the Sequence Identifiers), fragments and variants thereof, fusion proteins comprising it, polynucleotides or oligonucleotides derived therefrom, antibodies or fragments thereof binding to the polypeptide, pharmaceutical compositions or vaccines comprising these products and their use in methods for inhibiting, monitoring or diagnosing the development of a prostate cancer, for removing tumor cells from a sample or for expanding and/or stimulating T-cells.

Inventions 2. to 439. Claims: 1-79 (all partially and as far as applicable)

As for subject 1. but concerning respectively SEQ IDs 1,4-106,109-111,115-171,173-175,177,179-305,307-315,326,328, 330,332-335,340-375,381,382 and 384-472.

INTERNATIONAL SEARCH REPORT

Information on patent family members

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PCT/JS 99/15838

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